

CRFE

6034-24 na
13

U.S. Sci. & Tech. Ref. Serv.

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 13:57:30 ; Search time 590.797 Seconds
(without alignments)
2597.742 Million cell updates/sec

Title: US-10-604-726A-6034
Perfect score: 24
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 1796954

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: gb_ph.*
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9: gb_un.*
10: gb_vi.*
11: gb_ov.*
12: gb_htg.*
13: gb_in.*
14: gb_om.*
15: gb_bai.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	15.8	65.8	24	2	AX443910 Sequence
2	15.8	65.8	25	2	AX447886 Sequence
3	14.6	60.8	24	2	AX538707 Sequence
4	13.8	57.5	22	2	AR036420 Sequence
5	13.8	57.5	22	2	I29861 Sequence
6	13.4	55.8	28	2	BD141786 Novel G p
7	13.4	55.8	28	2	BD173668 Novel phy
8	13.4	55.8	28	2	BD181737 Novel G p
9	13.2	55.0	25	2	AR148541 Sequence
10	13.2	55.0	25	2	I62320 Sequence
11	13	54.2	17	2	AX215297 Sequence
12	13	54.2	17	2	AX215298 Sequence
13	13	54.2	17	2	AX215299 Sequence
14	13	54.2	17	2	AX215300 Sequence
15	13	54.2	20	2	AX298773 Sequence
16	13	54.2	27	2	AX347840 Sequence
17	12.8	53.3	19	2	AR069252 Sequence
18	12.8	53.3	19	2	CS101953 Sequence

19	12.8	53.3	19	2	CS102090 Sequence
20	12.8	53.3	25	2	AR240243 Sequence
21	12.6	52.5	19	2	AR628705 Sequence
22	12.6	52.5	20	2	AR100388 Sequence
23	12.6	52.5	20	2	AR150043 Sequence
24	12.6	52.5	20	2	BD227916 Antisense
25	12.6	52.5	20	2	AR442443 Sequence
26	12.6	52.5	20	8	AB213914 Synthetic
27	12.6	52.5	21	2	AR231257 Sequence
28	12.6	52.5	22	2	CS020856 Sequence
29	12.6	52.5	25	2	AR404657 Sequence
30	12.6	52.5	26	5	S75471 rhodopsin {
31	12.6	52.5	27	2	DD210483 GENOMIC S
32	12.6	52.5	28	2	AR534679 Sequence
33	12.6	52.5	28	2	AX004269 Sequence
34	12.6	52.5	30	2	AR139887 Sequence
35	12.6	52.5	30	2	AR139924 Sequence
36	12.6	52.5	30	2	AR167531 Sequence
37	12.6	52.5	30	2	AR167568 Sequence
38	12.6	52.5	30	2	AX924030 Sequence
39	12.6	52.5	30	2	BD084559 Recombina
40	12.6	52.5	30	2	BD084596 Recombina
41	12.6	52.5	30	2	BD250400 Methods f
42	12.6	52.5	30	2	AR234255 Sequence
43	12.6	52.5	30	2	AR234292 Sequence
44	12.6	52.5	30	2	AR238589 Sequence
45	12.6	52.5	30	2	AR476172 Sequence

ALIGNMENTS

RESULT 1
AX443910
LOCUS AX443910 24 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 365 from Patent WO0216649.
ACCESSION AX443910
VERSION AX443910.1 GI:21691188
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Gunderson, K.
TITLE Probes and decoder oligonucleotides
JOURNAL Patent: WO 0216649-A 365 28-FEB-2002;
Illumina, Inc. (US)
FEATURES
Location/Qualifiers
source
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."

ORIGIN

Query Match 65.8%; Score 15.8; DB 2; Length 24;
Best Local Similarity 73.7%; Pred. No. 6.2e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 GAGAGGGCGGUAAGGC 20
DB 4 GAGAGCGGTGTTAAGC 22

RESULT 2
AX447886
LOCUS AX447886 25 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 4341 from Patent WO0216649.
ACCESSION AX447886
VERSION AX447886.1 GI:21696785
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct

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CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (1). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
XX
SQ Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 18.6%; Score 15.8; DB 6; Length 24;
Best Local Similarity 73.7%; Pred. No. 5.9e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 16 GAGAGGGCGUGUUAAGGC 34
||||| :|||
Db 4 GAGAGGGCGTGTGTTAAGGC 22

RESULT 11
ABQ11043/c
ID ABQ11043 standard; DNA; 24 BP.

XX AC ABQ11043;
XX DT 11-JUN-2002 (first entry)
XX DE Oligonucleotide adapter/capture probe 11034.

XX KW Oligonucleotide array; adapter sequence; probe; ss.

XX OS Synthetic.

XX PN WO200216649-A2.

XX PD 28-FEB-2002.

XX PF 27-AUG-2001; 2001WO-US026519.

XX PR 25-AUG-2000; 2000US-0227948P.

XX PR 29-AUG-2000; 2000US-0228854P.

XX PA (ILLU-) ILLUMINA INC.

XX PI Gunderson K;

XX PS WPI; 2002-292068/33.

XX PT Array comprising adapter sequences useful for immobilizing or detecting a
XX target nucleic acid sequence, has different addresses comprising
XX different specific capture probes.

XX PS Claim 1; Page 225; 261pp; English.

XX CC The invention relates to an oligonucleotide array (1) comprising at least
XX 25 different addresses (adapter sequences) with each comprising a
XX different capture probe selected from a group consisting of the sequences
XX given in ABQ00010-ABQ13409. (1) is useful for immobilizing a target
XX nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
XX ABQ13409) to a target nucleic acid to form a modified target nucleic acid
XX and contacting the modified target nucleic acid with (1). The steps of
XX above method is useful for detecting a target nucleic acid, which further
XX comprises detecting the presence of the modified target nucleic acid
XX

SQ Sequence 24 BP; 5 A; 10 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 18.6%; Score 15.8; DB 6; Length 24;
Best Local Similarity 73.7%; Pred. No. 5.9e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Db 21 GAGAGGGCGTGTGTTAAGGC 3

RESULT 12
ABQ12538
ID ABQ12538 standard; DNA; 25 BP.

XX AC ABQ12538;

XX DT 11-JUN-2002 (first entry)

XX DE Oligonucleotide adapter/capture probe 12529.

XX KW Oligonucleotide array; adapter sequence; probe; ss.

XX OS Synthetic.

XX PN WO200216649-A2.

XX PD 28-FEB-2002.

XX PF 27-AUG-2001; 2001WO-US026519.

XX PR 25-AUG-2000; 2000US-0227948P.

XX PR 29-AUG-2000; 2000US-0228854P.

XX PA (ILLU-) ILLUMINA INC.

XX PI Gunderson K;

XX PS WPI; 2002-292068/33.

XX PT Array comprising adapter sequences useful for immobilizing or detecting a
XX target nucleic acid sequence, has different addresses comprising
XX different specific capture probes.

XX PS Claim 1; Page 244; 261pp; English.

XX CC The invention relates to an oligonucleotide array (1) comprising at least
XX 25 different addresses (adapter sequences) with each comprising a
XX different capture probe selected from a group consisting of the sequences
XX given in ABQ00010-ABQ13409. (1) is useful for immobilizing a target
XX nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
XX ABQ13409) to a target nucleic acid to form a modified target nucleic acid
XX and contacting the modified target nucleic acid with (1). The steps of
XX above method is useful for detecting a target nucleic acid, which further
XX comprises detecting the presence of the modified target nucleic acid
XX

SQ Sequence 25 BP; 7 A; 2 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 18.6%; Score 15.8; DB 6; Length 25;
Best Local Similarity 73.7%; Pred. No. 6e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 16 GAGAGGGCGUGUUAAGGC 34

Db 5 GAGAGGGCGTGTGTTAAGGC 23

RESULT 13

ABQ12579/c

ID ABQ12579 standard; DNA; 25 BP.

XX AC ABQ12579;

XX DT 11-JUN-2002 (first entry)

XX DE Oligonucleotide adapter/capture probe 12570.

XX KW Oligonucleotide array; adapter sequence; probe; ss.

XX OS Synthetic.

XX PN WO200216649-A2.

XX PD 28-FEB-2002.

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
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Run on: October 16, 2006, 14:22:20 ; Search time 1299 Seconds
(without alignments)
3889.027 Million cell updates/sec
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Perfect score: 79
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Searched: 6366136 segs, 31973710525 residues
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Minimum DB seq length: 0
Maximum DB seq length: 100
Post-processing: Minimum Match 0%
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Listing first 45 summaries

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				7: gb_sts:*			
				8: gb_sy:*			
				9: gb_un:*			
				10: gb_vi:*			
				11: gb_ov:*			
				12: gb_htg:*			
				13: gb_in:*			
				14: gb_om:*			
				15: gb_ba:*			
<p>Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.</p>							
SUMMARIES							
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1	23.6	29.9	97	2	AX184498	Sequence	
2	20.2	25.6	49	2	AX772410	Sequence	
C 3	20	25.3	93	2	AX987628	Sequence	
C 4	20	25.3	93	2	BD122487	EST and e	
C 5	20	25.3	93	2	AR426934	Sequence	
C 6	19.8	25.1	63	2	E08253	linker. 9/1	
C 7	19.8	25.1	92	14	AY753641	Sus scrofa	
C 8	19.4	24.6	97	2	AR165723	Sequence	
C 9	19.4	24.6	97	2	AR304919	Sequence	
C 10	19.2	24.3	51	2	BD034273	Sequence	
C 11	19.2	24.3	51	2	AR734534	Sequence	
C 12	19.2	24.3	51	2	AX898740	Sequence	
C 13	19.2	24.3	100	6	RXU12530	Sequence	
14	19	24.1	65	2	E08252	linker. 9/1	
C 15	19	24.1	65	2	AX184576	Sequence	
C 16	19	24.1	85	7	BX294351	Arabidops	
17	18.8	23.8	39	2	A86879	Sequence 19	
18	18.8	23.8	39	2	BD070385	Factor X-	

19	18.8	23.8	39	2	AR340859	Sequence	
20	18.8	23.8	54	2	AR118827	Sequence	
21	18.8	23.8	72	2	CS254876	Sequence	
22	18.8	23.8	79	2	AR126073	Sequence	
23	18.8	23.8	81	10	AF473711	Hepatitis	
24	18.6	23.5	55	2	BD270121	Method of	
25	18.6	23.5	65	2	CQ534358	Sequence	
26	18.6	23.5	69	6	MMTRB138	Mouse mRNA	
27	18.6	23.5	74	5	HUMDYSTR	Human DNA t	
28	18.6	23.5	94	2	CQ080813	Sequence	
29	18.6	23.5	94	2	CQ115279	Sequence	
30	18.6	23.5	94	2	CQ154107	Sequence	
31	18.6	23.5	94	2	CQ186687	Sequence	
32	18.6	23.5	94	2	CQ237346	Sequence	
33	18.6	23.5	94	2	CQ274971	Sequence	
34	18.6	23.5	94	2	CQ311944	Sequence	
35	18.6	23.5	94	2	CQ349319	Sequence	
36	18.6	23.5	100	2	AX929271	Sequence	
37	18.6	23.5	100	6	RNU12526	Rattus norv	
38	18.4	23.3	62	2	AR166135	Sequence	
39	18.4	23.3	62	2	AR235763	Sequence	
40	18.4	23.3	62	2	AR236505	Sequence	
41	18.4	23.3	62	2	AR279563	Sequence	
42	18.4	23.3	65	2	BD035476	Sequence	
43	18.4	23.3	65	2	AR735737	Sequence	
44	18.4	23.3	65	2	AX899943	Sequence	
45	18.4	23.3	81	2	CQ432140	Sequence	

ALIGNMENTS

RESULT 1
AX184498
LOCUS AX184498 97 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 193 from Patent WO0142467.
ACCESSION AX184498
VERSION AX184498.1 GI:15135853
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Schlegel, R., Deeds, J., Berger, A. and Zhao, X.
TITLE Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
JOURNAL Patent: WO 0142467-A 193 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)
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QY		16		GACGAGCGCGCUGCGCCCUAAUUGACUUGCGGCGUUAUUGUCUCCUUGCCAC 75	
Db		6		GCCGAGGTACGCGGGCGGTGNAGTAGGCTCGTCTCGGNTTTCTCTCTCTCGCTAA 65	
QY		76		CUCC 79	
Db		66		CGCC 69	
RESULT 2		AX772410		linear PAT 02-JUL-2003	
LOCUS		AX772410		49 bp DNA linear PAT 02-JUL-2003	

DEFINITION Sequence 200 from Patent WO03042407.
ACCESSION AX772410
VERSION AX772410.1 GI:32438983
KEYWORDS
SOURCE
ORGANISM Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1
AUTHORS Dickson,B., Berger,J., Suzuki,T. and Knoblich,J.
TITLE Method for identifying therapeutic targets by use of genetic
screens in drosophila melanogaster
JOURNAL Patent: WO 03042407-A 200 22-MAY-2003;
BOEHRINGER INGELHEIM INTERNATIONAL GMBH; CD Patents (DE)

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Db 6 CCGCTTTGTCCTCATTTAACTTCGGGTTCG 38

RESULT 3
AX987628/c
LOCUS AX987628 93 bp DNA linear PAT 15-JAN-2004
DEFINITION Sequence 18431 from Patent EP1104808.
ACCESSION AX987628
VERSION AX987628.1 GI:40993768
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1
AUTHORS Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y.
TITLE ESTs and encoded human proteins
JOURNAL Patent: EP 1104808-A 18431 06-JUN-2001;
Genset (FR)

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Db 58 GCGCGGGGAGACGAGCGGCTCAGGCCCTGCAGT 23

RESULT 4
BD122487/c
LOCUS BD122487 93 bp DNA linear PAT 18-SEP-2002
DEFINITION EST and encoded human protein.
ACCESSION BD122487
VERSION BD122487.1 GI:23217432
KEYWORDS JP 2002010789-A/14564.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1 (bases 1 to 93)
AUTHORS Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
TITLE EST and encoded human protein
JOURNAL Patent: JP 2002010789-A 14564 15-JAN-2002;
GENSET CORP

COMMENT OS Homo sapiens (human)
PN JP 2002010789-A/14564
PD 15-JAN-2002
PF 07-AUG-2000 JP 2000280989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
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FH Key, feature 63. .84
FT misc_feature 83.
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Query Match 25.3%; Score 20; DB 2; Length 93;
Best Local Similarity 63.9%; Pred. No. 3e+04;
Matches 23; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 5 GCGCGGGGAGACGAGCGGCUUGGCCCUUAUU 40
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Db 58 GCGCGGGGAGACGAGCGGCTCAGGCCCTGCAGT 23

RESULT 5
AR426934/c
LOCUS AR426934 93 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 18431 from patent US 6639063.
ACCESSION AR426934
VERSION AR426934.1 GI:40182044
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 93)
AUTHORS Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.
TITLE EST's and encoded human proteins
JOURNAL Patent: US 6639063-A 18431 28-OCT-2003;
Genset S.A.;;
WOX;

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Matches 23; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

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RESULT 6
E08253/c
LOCUS E08253 63 bp DNA linear PAT 29-SEP-1997

[illegible]

TITLE	JOURNAL				
Expressed sequence tags and encoded human proteins Patent: US 6783961-A 14603 31-AUG-2004; Genset S.A.; PRX;					
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LOCUS	AX898740	51 bp	DNA	linear	PAT 18-DEC-2003
DEFINITION	Sequence 14603 from Patent EP1033401.				
ACCSSION	AX898740				
VERSION	AX898740.1 GI:40053653				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens (human)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 Dumas Milne Edwards J.B., Duclert A. and Giordano J.Y. Auteurs Expressed sequence tags and encoded human proteins Journal Patent: EP 1033401-A 14603 06-SEP-2000; Genset (FR)				
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Matches	24; Conservative 3; Mismatches 13; Indels 0; Gaps 0;				
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RNU12530					
LOCUS	RNU12530	100 bp	mRNA	linear	ROD 21-JUL-1995
DEFINITION	Rattus norvegicus ultraviolet B radiation-activated UV126 mRNA, partial sequence.				
ACCSSION	U12530				
VERSION	U12530.1 GI:902953				
KEYWORDS	Rattus norvegicus (Norway rat)				
SOURCE	Rattus norvegicus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Murinae; Rattus.				
REFERENCE	1 Rosen C.F., Poon R. and Drucker D.J. Authors Ultraviolet B radiation-activated genes induced by transcriptional Title and posttranscriptional mechanisms in rat keratinocytes Unpublished Reference 2 (bases 1 to 100) Rosen C.F. Direct Submission Title				

JOURNAL	Submitted (21-JUL-1994)	Cheryl F. Rosen, Medicine, University of Toronto, 100 College Street, Room 317, Toronto, Ontario, M5G 1L5, Canada
FEATURES	source	1. .100 Location/Qualifiers /organism="Rattus norvegicus" /mol_type="mRNA" /strain="Sprague-Dawley" /db_xref="taxon:10116" /clone="UV126T7" /cell_type="keratinocyte" /dev_stage="newborn" 1. .100 /gene="UV126" <1. .>100 /genes="UV126"
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	mRNA	
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Best Local Similarity	47.5%;	Pred. No. 6e+04;
Matches	19; Conservative	8; Mismatches 13; Indels 0; Gaps 0;
Qy	40	UGUACUUCGGGCGUAGUUGUCUCCUUCGCCACCUCC 79
Db	52	TCTATGGCGAGCTGTACGTGCTCTCCCGCCCCCTCC 91
RESULT 14		
LOCUS	E08252	65 bp DNA linear PAT 29-SEP-1997
DEFINITION	linker.	
ACCESSION	E08252	
VERSION	E08252.1	GI:2176373
KEYWORDS	JP 1994279497-A/11.	
SOURCE	unidentified	
ORGANISM	unclassified sequences.	
REFERENCE	1 (bases 1 to 65)	
AUTHORS	Doi, T., Iwasaki, A., Saino, S., Kimura, S. and Oguchi, M.	
TITLE	THROMBIN-BINDING SUBSTANCE AND ITS PRODUCTION	
JOURNAL	Patent: JP 1994279497-A 11 04-OCT-1994;	
COMMENT	KOWA CO	
	OS None	
	OC Artificial sequences.	
	PN JP 1994279497-A/11	
	PD 04-OCT-1994	
	PF 25-NOV-1991 JP 1991308976	
	PI 30-NOV-1990 JP 90P 335720, 25-FEB-1991 JP 91P 30271 PI	
	DR TAKESHI, IWASAKI AKIO, SAINO SUKEYUKI, KIMURA SHIGERU, PI	
	OGUCHI MASAO	
	PC C07K13/00, A61K37/02, C12N1/21, C12N5/10, C12N15/12, C12N15/70, PC	
	C12P21/02, (C12N1/21, C12R1:19), (C12P21/02, C12R1:91);	
	CC strandedness: Single;	
	CC topology: Linear;	
	FH Key	
	FT Location/Qualifiers	
	FT source	1. .65
	FT /organism='Artificial sequences'.	
FEATURES	source	Location/Qualifiers 1. .65 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"
ORIGIN		
Query Match	24.1%;	Score 19; DB 2; Length 65;
Best Local Similarity	62.9%;	Pred. No. 6.7e+04;
Matches	22; Conservative	3; Mismatches 10; Indels 0; Gaps 0;
Qy	3	AGGCGGGGAGAGACGAGCGGCGUCUGGCCCUUA 37
Db	30	AGCTCAGCAGCGAGCGGCGGCTGTGGCGACTGA 64

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:22:19 ; Search time 302 Seconds
(without alignments)
1823.866 Million cell updates/sec

Title: US-10-604-726A-5135

Perfect score: 79

Sequence: 1 ggagggcggggagagacga.....ucucuccuucgccaccucc 79

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 5647924

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8.*

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- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*
- 15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23.6	29.9	97	4	Aah68919 Human cer
2	23	29.1	87	6	ABL75509
3	20.4	25.8	86	2	Aax54100 RANTES re
4	20.4	25.8	86	3	Aax33544 Low adeno
5	20.4	25.8	86	3	Aaf19666 Human MIP
6	20.4	25.8	86	10	ABZ295360
7	19.8	25.1	90	2	Aat69848 Open circ
8	19.8	25.1	93	6	Abq90817 M. capsul
9	19.6	24.8	86	11	ABD19191 Human RAN
10	19.4	24.6	97	9	ADA22018 HGF aptam
11	19.2	24.3	51	3	AAC10528 Human sec
12	19.2	24.3	80	12	ADM79864 DNA ligan
13	19.2	24.3	87	8	ABX51458 Bovine ES
14	19	24.1	65	4	Aah68997 Human cer
15	19	24.1	97	14	ADX69632 Human Gnt
16	19	24.1	97	14	ADZ59082 Human Gnt
17	18.8	23.8	39	2	AAV56769 Human Fac
18	18.8	23.8	72	6	AAD30987 Schizosac

C	19	18.8	23.8	72	6	AAD31044
	20	18.8	23.8	79	4	Aaf70953 BFGF DNA
	21	18.8	23.8	80	2	Aat00367 Family 4
C	22	18.6	23.5	55	3	Aaa09070 Sense pri
	23	18.6	23.5	65	6	ABN31245 Rat splic
C	24	18.6	23.5	80	12	ADM95117 Rat antis
	25	18.6	23.5	94	4	AAL26680 Probe #16
C	26	18.6	23.5	94	4	ABA74927 Human foe
	27	18.6	23.5	94	4	AAI55452 Probe #24
C	28	18.6	23.5	94	4	ABA39617 Probe #18
	29	18.6	23.5	94	4	AAK49572 Human bon
C	30	18.6	23.5	94	4	AAK23422 Human bra
	31	18.6	23.5	94	4	ABS49195 Human liv
C	32	18.6	23.5	94	6	ABS23058 Human gen
	33	18.6	23.5	98	12	ADG99544 Kidney di
C	34	18.6	23.5	100	8	ACD73164 E. coli K
	35	18.4	23.3	62	2	AAX59388 Saccharom
	36	18.4	23.3	65	3	AAC11731 Human sec
	37	18.4	23.3	80	12	ADP49484 Oligonucl
	38	18.4	23.3	81	4	AAL24704 Human bre
	39	18.4	23.3	82	4	AAL24473 Human bre
	40	18.4	23.3	90	6	ABK36475 HCV DNA e
C	41	18.4	23.3	93	4	Aah71852 Human cer
	42	18.4	23.3	93	4	Aah68985 Human cer
C	43	18.4	23.3	94	4	Aah72271 Human cer
	44	18.2	23.0	50	13	ADU25177 Retroelem
	45	18.2	23.0	50	13	ADU22644 Human tra

ALIGNMENTS

RESULT 1
AAH68919
ID AAH68919 standard; cDNA; 97 BP.

AC AAH68919;

DT 19-SEP-2001 (first entry)

DE Human cervical cancer marker nucleic acid 193.

XX Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.

OS Homo sapiens.

PN WO200142467-A2.

PD 14-JUN-2001.

PF 08-DEC-2000; 2000WO-US033312.

PR 08-DEC-1999; 99US-0169681P.

PR 21-DEC-1999; 99US-0171350P.

PR 14-MAR-2000; 2000US-0189315P.

PR 12-MAY-2000; 2000US-0203791P.

PR 09-JUN-2000; 2000US-0210600P.

PR 21-JUL-2000; 2000US-0220114P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Deeds J, Berger A, Zhao X;

DR WPI; 2001-375006/39.

XX New isolated nucleic acid for diagnosing and treating cervical cancer and
PT for assessing and detecting compounds for treating the cancer.
XX Claim 1; Page 137; 1051pp; English.
XX The invention relates to novel genes (AAH68727-AAH73383) associated with
CC cervical cancer with cytostatic activity. The nucleic acids and encoded
CC polypeptides are useful; to assess if a patient is afflicted with


```
XX Synthetic.
OS Homo sapiens.
XX
XX WO9719193-A2.
XX
XX PD 29-MAY-1997.
XX
XX PF 21-NOV-1996; 96WO-US018812.
XX
XX PR 21-NOV-1995; 95US-00563912.
XX
XX PR 01-MAY-1996; 96US-0016677P.
XX
XX (UYA ) UNIV YALE.
XX
XX PI Lizardi PM, Caplan M;
XX
XX DR WPI; 1997-298125/27.
XX
XX Unimolecular segment amplification method for amplifying nucleic acids -
PT uses rolling circle mechanism of amplification, useful for disease-
PT associated genetic mutation(s).
XX
XX Example 6; Page 82; 149pp; English.
XX
XX This sequence represents a probe to test the method of the invention. The
CC method of the invention is for amplifying a nucleic acid molecule. It
CC comprises mixing at least one rolling circle replication primer (RCRP)
CC with at least one amplification target circle (ATC) which comprises a
CC single stranded circular DNA containing a region complementary to the
CC RCRP, such that the RCRP hybridises to the ATC and mixing the ATC-RCRP
CC complex with a DNA polymerase and incubating such that a tandem sequence
CC DNA is formed. The method, designated unimolecular segment amplification,
CC is used for detecting specific sequences with high speed and sensitivity.
CC It is especially useful for detecting mutations in genes where numerous
CC distinct mutations are associated with a disease or where mutations in
CC multiple genes are involved. The method is isothermal and provides a
CC simple, consistent and quantitative detection of multiple target
CC molecules as the amplification occurs not in cycles but as a single
CC continuous reaction. The method is strictly quantitative as the
CC amplification step is linear and is catalysed by a highly processive
CC enzyme
XX
XX Sequence 90 BP; 24 A; 18 C; 12 G; 36 T; 0 U; 0 Other;
SQ
Query Match 25.1%; Score 19.8; DB 2; Length 90;
Best Local Similarity 35.9%; Pred. No. 4.8e+03;
Matches 14; Conservative 13; Mismatches 12; Indels 0; Gaps 0;
QY 33 CCUUAUUGUACUUCGGGUCGUUUGUCUUCUUCUUCG 71
Db 7 CTTTATGGTTCTCTGACTCGTCGTCGTCGCTTAC 45
RESULT 8
ABQ90817
ID ABQ90817 standard; DNA; 93 BP.
XX
XX AC ABQ90817;
XX
XX DT 01-OCT-2002 (first entry)
XX
XX DE M. capsulatus gene #802 for DNA array.
XX
XX KW Micro array; gene; ds; differential expression; gene expression.
XX
XX OS Methylococcus capsulatus.
XX
XX PN WO200255655-A2.
XX
XX PD 18-JUL-2002.
XX
XX PF 14-JAN-2002; 2002WO-NO000019.
```

```
XX 12-JAN-2001; 2001NO-00000235.
PR 12-JAN-2001; 2001NO-00000235.
XX
XX (UNIP-) UNIFOB STIFTELSEN UNIV BERGEN.
PA (TIGR-) TIGR.
XX
XX Birkeland NK, Eidhammer I, Jonassen I, Jensen HB, Lien T;
PI Lillehaug JR, Lossius I, Eisen JA, Fraser CM, Durkin AS;
PI Salzberg SL;
XX
XX WPI; 2002-557818/59.
XX
XX Novel DNA array useful for determining differential expression of
PT Methylococcus capsulatus genes, comprises polynucleotides or
PT oligonucleotides representative for a selective number of Methylococcus
PT capsulatus genes.
XX
XX Claim 14; Page 359; 678pp; English.
XX
XX The invention relates to a novel DNA array giving a representation of a
CC number of Methylococcus capsulatus genes. The method of the invention is
CC useful for determination of the differential expression of the genes of
CC M. capsulatus, and for studying gene expression on a genomic scale and in
CC gene expression assays of M. capsulatus genes. The sequences shown in
CC ABQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the
CC invention
XX
XX Sequence 93 BP; 17 A; 30 C; 26 G; 20 T; 0 U; 0 Other;
SQ
Query Match 25.1%; Score 19.8; DB 6; Length 93;
Best Local Similarity 51.6%; Pred. No. 4.8e+03;
Matches 16; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
QY 49 GGCUCGUUUGUCUUCUUCUUCUUCUUCUUCUUC 79
Db 3 GGCAGCTTTTTCACCTCTTCGTTACCGCC 33
RESULT 9
ABD19391
ID ABD19391 standard; DNA; 86 BP.
XX
XX AC ABD19391;
XX
XX DT 29-JUL-2004 (first entry)
XX
XX DE Human RANTES DNA fragment 1224.
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200285309-A2.
XX
XX PD 31-OCT-2002.
XX
XX PF 23-APR-2002; 2002WO-US013143.
XX
XX PR 24-APR-2001; 2001US-0286036P.
XX
XX (EPIC-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandraagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
```

DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 10602; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 86 BP; 0 A; 26 C; 26 G; 19 T; 0 U; 15 Other;
Query Match 24.8%; Score 19.6; DB 11; Length 86;
Best Local Similarity 38.6%; Pred. No. 5.5e+03;
Matches 27; Conservative 7; Mismatches 36; Indels 0; Gaps 0;
QY 4 GGCGGGGAGAGACGAGCGGCGUCUGGCCCCUUAUUGUACUUGCGGCGUUAUUGUCUC 63
DB 1 GNGGGGCGCGNGTGGGCGCCNNGCCCTCTCTGTCNCTTCTGCGCGGNGTTGCNT 60
QY 64 UCUUUGCC 73
DB 61 CCCNTNGTC 70
RESULT 10
ADA22018/C
ID ADA22018 standard; RNA; 97 BP.
XX
AC ADA22018;
XX
XX 20-NOV-2003 (first entry)
DT
XX HGF aptamers-associated RNA sequence #99.
DE
XX ss; hypotensive; antiarteriosclerotic; cardiant; antirheumatic;
KW antiarthritic; gene therapy; cyostatic; RNA aptamer;
KW hepatocyte growth factor/scatter factor; HGF; HGF receptor; c-met;
KW ligand; tumour; angiogenesis; vascular endothelial factor; VEGF;
KW basic fibroblast growth factor; hypertension; arteriosclerosis;
KW myocardial infarction; rheumatoid arthritis; motogenesis; SELEX;
KW systematic evolution of ligands by exponential enrichment.
XX

OS Unidentified.
XX
PN US2003049644-A1.
XX
PD 13-MAR-2003.
XX
XX 04-FEB-2002; 2002US-00066960.
XX
XX 10-JUN-1991; 91US-00714131.
PR 06-JUN-1995; 95US-00469609.
PR 29-SEP-1995; 95US-00536428.
PR 29-JUL-1999; 99US-00364539.
PR 10-FEB-2000; 2000US-00502344.
XX
XX (GILE-) GILEAD SCI INC.
XX
XX Rabin R, Lochrie M, Janjic N, Gold L;
PI WPI; 2003-567063/53.
XX
XX New nucleic acid ligands to hepatocyte growth factor/scatter factor or c-
PT met, diagnostic and therapeutic agents for hypertension,
PT arteriosclerosis, myocardial infarction and rheumatoid arthritis.
XX
XX Disclosure; Page 101; 157pp; English.
XX
XX The invention relates to a purified and isolated non-naturally occurring
CC nucleic acid ligand (an RNA aptamer) to hepatocyte growth factor/scatter
CC factor (HGF) or the HGF receptor, c-met. The ligand comprises a sequence
CC selected from 148 fully defined sequences of 17-101 bp given in the
CC specification. Also included are a method of treating a tumour by
CC administering the aptamer, a method for inhibiting angiogenesis by administering the
CC individual, a method for inhibiting angiogenesis by administering the
CC aptamer (and a pharmaceutical excipient), a method for treating a disease
CC in which elevated HGF is a causative factor (by administering a nucleic
CC acid ligand to HGF) and a method for inhibiting tumour development
CC (comprising administering a nucleic acid ligand to HGF in combination
CC with a nucleic acid ligand to vascular endothelial factor (VEGF) and/or
CC basic fibroblast growth factor, nucleic acid ligands to at least 2 growth
CC factors, nucleic acid ligands to at least 2 receptors of growth factors
CC or nucleic acid ligands to one or more receptors of growth factors). The
CC combination with nucleic acid ligands to one or more growth factors. The
CC aptamers comprise 2'-F (2'-fluoro) modified ribonucleic acids. The
CC nucleic acid ligands are useful as diagnostic and therapeutic agents for
CC hypertension, arteriosclerosis, myocardial infarction and rheumatoid
CC arthritis. Nucleic acid ligands to HGF and c-met are used to measure the
CC levels of these proteins in an individual to obtain prognostic and
CC diagnostic information. Nucleic acid ligands that inhibit HGF/c-met
CC interaction are useful for inhibiting tumourigenesis by inhibiting
CC angiogenesis and motogenesis. The high-affinity nucleic acid ligands
CC containing modified nucleotides confer improved characteristics on the
CC ligand, such as improved in vivo stability or improved delivery
CC characteristics. The aptamers were identified using the technique of
CC SELEX (systematic evolution of ligands by exponential enrichment) using
CC libraries of aptamers with either 30 or 40 randomised nucleotides (30N or
CC 40N) surrounded by a constant region. The present sequence is an RNA
CC sequence included in the sequence listing but not mentioned anywhere else
CC in the specification.
XX
SQ Sequence 97 BP; 42 A; 18 C; 27 G; 0 T; 7 U; 3 Other;
Query Match 24.6%; Score 19.4; DB 9; Length 97;
Best Local Similarity 31.1%; Pred. No. 6.7e+03;
Matches 19; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
QY 19 GAGCGGCGUGGCCCCUUAUUGUACUUGCGGCGUUAUUGUCUCUCCGCCACCUC 78
DB 90 GTGAGCCCTCTGTCGAATCTTACTCTGCTTGTGTTGTTGTCGCGGCCCT 31
QY 79 C 79
DB 30 C 30

RESULT 11
AAC10528/c
ID AAC10528 standard; cDNA; 51 BP.
XX AAC10528;
AC AAC10528;
XX 06-OCT-2000 (first entry)
DT XX
DE XX
DE Human secreted protein 5' EST, SEQ ID NO: 14603.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
XX 06-SEP-2000.
PD XX
XX 21-FEB-2000; 2000EP-00200610.
PF XX
PR 26-FEB-1999; 99US-0122487P.
XX
XX (GEST) GENSET.
PA Dumas Milne Edwards J, Duclert A, Giordano J;
PI WPI; 2000-500381/45.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
PT
PS Claim 1; SEQ ID NO 14603; 71pp + Sequence Listing; English.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors
XX
XX Sequence 51 BP; 5 A; 23 C; 19 G; 4 T; 0 U; 0 Other;
SQ
Query Match 24.3%; Score 19.2; DB 3; Length 51;
Best Local Similarity 60.0%; Pred. No. 6.9e+03;
Matches 24; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
QY 1 GGAGGCGGGGAGACGACGAGCGGCGUCUGGCCCCCUAAUU 40
DB 47 GGCGGCGGGCGGCGGCGGACGACGCGGCTCAGGCCCTGCAGT 8
RESULT 12
ADM79864
ID ADM79864 standard; DNA; 80 BP.
XX
AC ADM79864;
XX
XX 03-JUN-2004 (first entry)
DT
DE DNA ligand identification-related aptamer DNA sequence SeqID6.
XX

KW CE-SELEX; capillary electrophoresis; ligand-enriched mixture;
KW antiasthmatic; cerebroprotective; anti-HIV; virucide;
KW analytical chemistry; in vivo imaging; biosensor; complex matrix;
KW affinity probe capillary electrophoresis; APCE; ELISA;
KW fibre-optic microarray biosensor; histological marker;
KW tumour microvessel; anthrax spore; cocaine; ds.
XX
OS Unidentified.
OS Synthetic.
XX
PN WO2003102212-A2.
XX
PD 11-DEC-2003.
XX
PF 29-MAY-2003; 2003WO-US016796.
XX
PR 31-MAY-2002; 2002US-0384709P.
PR 15-MAY-2003; 2003US-0470750P.
XX
XX (MINU) UNIV MINNESOTA.
PA
XX Bowser MT, Mendonsa SD;
PI WPI; 2004-043125/04.
XX
XX Identifying nucleic acid ligand of target molecule from mixture
PT comprising single stranded nucleic acids having region of randomized
PT sequence by contacting mixture with target molecule, amplifying affinity
PT nucleic acids.
XX
PS Claim 27; SEQ ID NO 6; 90pp; English.
XX
XX This invention relates to a novel method (CE-SELEX, Capillary
CC Electrophoresis-Systematic Evolution of Ligands by Exponential
CC enrichment) of identifying nucleic acid ligands of a target molecule from
CC a candidate mixture comprised of single stranded nucleic acids each
CC having a region of randomized sequence by contacting the mixture with the
CC target molecule, where nucleic acids having affinity to the target
CC molecule are partitioned from the mixture by capillary electrophoresis,
CC amplifying increased affinity nucleic acids to yield a ligand-enriched
CC mixture of nucleic acids. The invention may be useful for the production
CC of compounds with an antiasthmatic, cerebroprotective, anti-HIV or
CC virucide activity. The method is useful for identifying nucleic acid
CC ligands of a target molecule from a candidate mixture comprised of single
CC stranded nucleic acids each having a region of randomized sequence.
CC Aptamers identified by the method are useful as a tool in analytical
CC chemistry, useful in wide range of diagnostic assays and as direct
CC benefits to many area of the research, including biomedical and health
CC research. Improved aptamers are useful in developing diagnostic assays,
CC for example as diagnostic markers in medical analysis, in vivo imaging
CC and biosensors. The aptamers are also useful in quantitating targets
CC present in complex matrices. The aptamers are used to develop high-
CC sensitivity affinity probe capillary electrophoresis (APCE) assays, in
CC ELISA type assays using enzyme-linked DNA aptamers. Thrombin aptamers may
CC be developed for using fibre-optic microarray biosensors. Aptamers
CC against transformed endothelial cells may be selected for use as
CC histological markers to identify tumour microvessels. Aptamers may be
CC developed for use in other aptamer-based assays, such as assays for
CC analytes ranging from anthrax spores to cocaine. Aptamers having improved
CC quality, improved binding efficiency and selectivity can be identified by
CC the method of the invention. The present sequence is that of an aptamer
CC DNA sequence which was identified using the method of the invention.
XX
SQ Sequence 80 BP; 17 A; 21 C; 21 G; 21 T; 0 U; 0 Other;

Query Match 24.3%; Score 19.2; DB 12; Length 80;
Best Local Similarity 35.9%; Pred. No. 7.5e+03;
Matches 23; Conservative 13; Mismatches 28; Indels 0; Gaps 0;
QY 6 GCGGCGGAGACGACGAGCGGCGUCUGGCCCCCUAAUUUUAUUAUUGGCGUCUUAUUGUCUC 65
DB 2 GCAGCACAGAGGTGAGTGTGTGACCGTTATTGTGCTCAGCATCCCCGGGCTAAC 61

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QY 66 CUVU 69
Db 62 CTAT 65

Query Match 24.3%; Score 19.2; DB 8; Length 87;
Best Local Similarity 37.5%; Pred. No. 7.7e+03;
Matches 15; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

RESULT 13
ID ABX51458 standard; cDNA; 87 BP.
XX
AC ABX51458;
XX
XX
DT 25-FEB-2003 (first entry)
XX
DE Bovine EST associated with lactation/muscle/fat deposition #1387.
XX
KW Bovine; ss; EST; expressed sequence tag; lactation; LMPD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX
XX Bos Taurus.
XX
XX US2002137160-A1.
XX
XX 26-SEP-2002.
XX
XX 26-OCT-2001; 2001US-00983965.
XX
XX 17-DEC-1998; 98US-0113678P.
XX
XX 15-DEC-1999; 99US-00465231.
XX
XX (BYAT/) BYATT J C.
XX
XX (MATH/) MATHIALAGAN N.
XX
XX (TAON/) TAO N.
XX
XX (WARR/) WARREN W C.
XX
XX Byatt JC, Mathialagan N, Tao N, Warren WC;
XX
XX WPI; 2003-102386/09.
XX
XX Purified nucleic acid molecules, useful for genome mapping, gene
XX identification and analysis, cattle breeding or preparation of constructs
XX for cattle gene expression and genetically improved cattle.
XX
XX Claim 2; SEQ ID NO 1387; 38pp; English.
XX
XX The invention relates to a purified nucleic acid molecule associated with
XX lactation or muscle and fat deposition (designated LMPD), derived from
XX cattle, and the LMPD nucleic acid can specifically hybridise to a second
XX nucleic acid molecule comprising any of 5912 nucleotide sequences,
XX appearing as ABX50072-ABX55983, or complements of them. Also included are
XX ; (1) a transformed cell having a nucleic acid comprising an LMPD nucleic
XX acid linked to a promoter and a 3', non-translated sequence that
XX functions in the cell to cause termination of transcription and addition
XX of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
XX (2) determining a level or pattern of a molecule in a bovine cell or
XX tissue comprising: (a) incubating a marker nucleic acid (comprising any
XX of the 5912 nucleic acid sequences or its complement or fragment) with a
XX complementary nucleic acid molecule obtained from the bovine cell or
XX tissue, where hybridisation between the marker nucleic acid and the
XX complementary nucleic acid permits the detection of the molecule; and (b)
XX detecting the level or pattern of the complementary nucleic acid, where
XX the detection of the complementary nucleic acid is predictive of the
XX level or pattern of the molecule. The LMPD nucleic acid is used for
XX determining a level or pattern of a molecule in a bovine cell or tissue.
XX It is useful for genome mapping, gene identification and analysis, cattle
XX breeding, preparation of constructs for use in cattle gene expression, or
XX for genetically improving cattle. The present sequence is one of the 5912
XX bovine LMPD EST (expressed sequence tag) nucleic acids. Note: The present
XX sequence was not shown in the specification but was obtained in
XX electronic format from the USPTO web site:
XX seqdata.uspto.gov/sequence.html?docId=20020137160
XX
XX Sequence 87 BP; 28 A; 28 C; 3 G; 28 T; 0 U; 0 Other;
```

```
QY 31 CCCUUAUUGUACUUCGGGCUUCGUUAUUGUCUCUCUUCUUC 70
Db 39 CCTCTTAATCTATATCTTACTCCAATTCACCTCCCTCTC 78

Query Match 24.3%; Score 19.2; DB 8; Length 87;
Best Local Similarity 37.5%; Pred. No. 7.7e+03;
Matches 15; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

RESULT 14
ID AAH68997 standard; cDNA; 65 BP.
XX
XX AAH68997;
XX
XX 19-SEP-2001 (first entry)
XX
XX Human cervical cancer marker nucleic acid 271.
XX
XX Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX
XX Homo sapiens.
XX
XX WO200142467-A2.
XX
XX 14-JUN-2001.
XX
XX 08-DEC-2000; 2000WO-US033312.
XX
XX 08-DEC-1999; 99US-0169681P.
XX
XX 21-DEC-1999; 99US-0171350P.
XX
XX 14-MAR-2000; 2000US-0189315P.
XX
XX 12-MAY-2000; 2000US-0203791P.
XX
XX 09-JUN-2000; 2000US-0210600P.
XX
XX 21-JUL-2000; 2000US-0220114P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Deeds J, Berger A, Zhao X;
XX
XX WPI; 2001-375006/39.
XX
XX New isolated nucleic acid for diagnosing and treating cervical cancer and
XX for assessing and detecting compounds for treating the cancer.
XX
XX Claim 1; Page 150; 1051pp; English.
XX
XX The invention relates to novel genes (AAH68727-AAH73383) associated with
XX cervical cancer with cytostatic activity. The nucleic acids and encoded
XX polypeptides are useful: to assess if a patient is afflicted with
XX cervical cancer or has a pre-malignant condition; to monitor the
XX progression of cervical cancer or a premalignant condition in a patient;
XX and to select and/or assess the efficacy of a compound or therapy for
XX inhibiting cervical cancer in a patient. The nucleic acids may also be
XX useful for gene therapy
XX
XX Sequence 65 BP; 19 A; 17 C; 19 G; 4 T; 0 U; 6 Other;

Query Match 24.1%; Score 19; DB 4; Length 65;
Best Local Similarity 37.5%; Pred. No. 8.5e+03;
Matches 15; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 40 UGUACUUCGGGCUUCGUUAUUGUCUCUCUUCGCGCACCUCC 79
Db 44 TTTTCTTCGTCMTCGGAANANTCTCTCTCTCGCTNNCGCC 5

RESULT 15
ID ADX69632 standard; DNA; 97 BP.
XX
XX ADX69632;
```

XX 05-MAY-2005 (first entry)
XX DE Human GntIII mutagenic forward PCR primer 1-97.
XX KW Antibody engineering; radioimmunotherapy;
XX KW antibody-dependent cellular toxicity;
KW n-acetyl glucosaminyl transferase III; ss; PCR; primer; Cytostatic;
KW immunotherapy; tumor; neoplasm; multiple myeloma; hematological disease;
KW immune disorder.
XX OS Homo sapiens.
OS Synthetic.
XX PN WO2005014651-A1.
XX PD 17-FEB-2005.
XX PF 11-AUG-2004; 2004WO-JP011812.
XX PR 11-AUG-2003; 2003JP-00207165.
XX PA (CHUS) CHUGAI SEIYAKU KK.
XX PI Tsuchiya M, Iijima S, Sugo I, Sugimoto M;
XX WPI; 2005-173081/18.
XX DR Anti-HM1.24 antibody useful for diagnosis of a tumor and useful as a
PT therapeutic agent for treating myeloma, comprises a modified sugar chain.
XX Example 9; SEQ ID NO 2; 58pp; Japanese.
XX The invention relates to an anti-HM1.24 (I) antibody which has a modified
CC sugar chain. Also included are an antibody composition, containing (I) in
CC which the sugar chain does not contain fucose and the relative ratio of
CC the sugar chain is 30% or more and producing the antibody. The modified
CC antibody is produced by culturing a host cell in which the ability of the
CC cell to add fucose in the sugar chain of the antibody, is deleted, and in
CC which the nucleic acid encoding the anti-HM1.24 antibody is introduced,
CC by culturing a host cell in which nucleic acid encoding N-acetyl
CC glucosamine transferase III (GnTIII) is introduced, or by culturing a
CC host cell having both deleted fucose addition ability and ability to
CC express N-acetyl glucosamine transferase III, and extracting the antibody
CC from the cultured solution. The antibody does not contain alpha-1,6 core
CC fucose and/or has a sugar chain having a bisecting N-acetylglucosamine
CC (GlcNAc) structure. The modified antibody is useful for diagnosis of a
CC tumor and is useful as a therapeutic agent for treating myeloma such as
CC multiple myeloma. The antibody-dependent cellular cytotoxicity (ADCC) of
CC the antibody) is enhanced by the sugar chain modification. The present
CC sequence is a PCR primer used to produce a mutant GntIII DNA.
XX Sequence 97 BP; 15 A; 34 C; 16 G; 32 T; 0 U; 0 Other;
Query Match 24.1%; Score 19; DB 14; Length 97;
Best Local Similarity 38.8%; Pred. No. 9.2e+03;
Matches 26; Conservative 11; Mismatches 30; Indels 0; Gaps 0;
QY 12 GAGAGACGACGCGCUCUGGCCCUUAUUGACUUGCGGCUUGUUCUUCUUCUG 71
DB 3 GAGACGCTACAGCTCTTTCTCTGATGTCGCGCGCTGTGCTATCTCTCTCT 62
QY 72 CCACCUC 78
DB 63 GCACCTTC 69

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:23:36 ; Search time 4326 Seconds
(without alignments)
1021.181 Million cell updates/sec

Title: US-10-604-726A-5135
Perfect score: 79
Sequence: 1 98agggcgggagagacga.....ucucuccuuccgccaccucc 79

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 853524

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	21.6	27.3	76 4 BX728792
2	21.2	26.8	84 1 AA414137
3	21.2	26.8	91 1 AI583881
4	20.8	26.3	91 1 AI269698
5	20.6	26.1	100 3 BQ382202
6	20.2	25.6	85 7 BF147704
7	20.2	25.6	100 1 AI616438
8	20.2	25.3	81 12 CC1831143
9	20.2	25.3	88 10 H55638
10	19.8	25.1	78 14 CT351516
11	19.8	25.1	83 13 CW115558
12	19.8	25.1	83 13 CW115559
13	19.6	24.8	71 13 CW020424
14	19.6	24.8	84 10 DT921192
15	19.6	24.8	85 1 AJ649396
16	19.6	24.8	89 1 AA437593
17	19.6	24.8	100 11 AZ769498
18	19.4	24.6	58 14 CR076775
19	19.4	24.6	71 9 DN441479

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

20	19.4	24.6	76	11	BZ381406
21	19.4	24.6	76	13	CW236987
22	19.4	24.6	78	10	H25883
23	19.4	24.6	84	13	CW067844
24	19.4	24.6	94	7	AV957037
25	19.4	24.6	100	8	CO167293
26	19.2	24.3	46	1	AI1360975
27	19.2	24.3	50	1	AUI05862
28	19.2	24.3	66	13	CW022621
29	19.2	24.3	78	14	DX045680
30	19.2	24.3	79	1	AI539851
31	19.2	24.3	89	13	DU099947
32	19.2	24.3	89	13	DU108469
33	19.2	24.1	51	14	CR289701
34	19.2	24.1	78	8	CR587313
35	19.2	24.1	79	11	AZ605020
36	19.2	24.1	85	11	AZ770277
37	19.2	24.1	91	1	AA691640
38	19.2	24.1	92	2	BM157107
39	19.2	24.1	98	6	AK192966
40	18.8	23.8	46	1	AA569383
41	18.8	23.8	61	4	CB046583
42	18.8	23.8	67	10	DY248960
43	18.8	23.8	73	5	CD945332
44	18.8	23.8	78	2	BQ029975
45	18.8	23.8	88	5	CF028477

ALIGNMENTS

RESULT 1
BX728792
LOCUS
DEFINITION BX728792 XGC-tadpole Xenopus tropicalis cDNA clone TTPA036j08 5',
mRNA sequence.
ACCESSION BX728792.1 GI:38401533
VERSION
KEYWORDS
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 76)
Cronin,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
Contact: Cronin MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE ID: TTPA036j08.pikSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett.
cDNA was oligo dt primed from 5ug of poly A+ RNA from tadpole
embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site_1: EcoRI; Site_2: NotI
Host: Escherichia coli DH10B.
Location/Qualifiers
1..76
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TTPA036j08"
/dev_stage="tadpole (stage 35-40)"
/lab_host="E. coli DH10B"
/clone_lib="XGC-tadpole"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dt primed from 5ug of poly A+ RNA from tadpole

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 91)
TITLE NCI/NIHDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute / National Institute of Neurological
 Disorders and Stroke, Brain Tumor Genome Anatomy Project
 (CGAP/BTCAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsb-x@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

FEATURES
 source
 1..91
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1998275"
 /tissue_type="tumor, 5 pooled (see description)"
 /lab_host="DH10B"
 /clone_lib="NCI-CGAP Brn35"
 /notes="Organ: Brain; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.33 kb. Tumor types include:
 meningioma, oligodendroglioma, astrocytoma (grade II),
 medulloblastoma, astrocytoma (grade IV). Life Technologies
 catalog #: 11544-012"

ORIGIN
 Query Match 26.3%; Score 20.8; DB 1; Length 91;
 Best Local Similarity 33.9%; Pred. No. 3.le+04;
 Matches 19; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

QY 24 GCUCUGCCCCUUAUUGUACUUGCGGUCUGAUUGUCUCUCCUUGCGCACCUCC 79
 | : ||||| : : : ||| : : : : : : : : : ||||| ||
Db 71 GTTTTCCCGCTGGTGTTTTGTGCGCCCTCGTACCCCTTTTCCCAACCC 16

RESULT 5
BQ382202
LOCUS BQ382202.1 GI:21057716
DEFINITION 100 bp mRNA linear EST 21-MAY-2002
 Ascaris suum male gut pAMP1 v2 Chiapelli McCarter
ACCESSION BQ382202.1
VERSION BQ382202.1
KEYWORDS Ascaris suum male gut pAMP1 v2 Chiapelli McCarter
SOURCE EST.
ORGANISM Ascaris suum (pig roundworm)
 Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida;
 Ascaridoidea; Ascarididae; Ascaris.
 1 (bases 1 to 100)
 McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
 Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
 Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
 Tagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
 Underwood, K., Stepcoe, M., Allen, M., Person, S., Swaller, T.,
 Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
 McCann, R., Waterston, R. and Wilson, R.
 The Washington Univ. Nematode EST Project, 1999

JOURNAL COMMENT

Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu

The library was constructed by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Dissected nematode tissues were provided by Dr. Alan Scott (ascott@jhph.edu) of the School of Public Health and Public Health at John Hopkins University in Baltimore, MD.
Seq primer: T7 from Gibco
High quality sequence stop: 99.

FEATURES

source	Location/Qualifiers
	1..100
	/organism="Ascaris suum"
	/mol_type="mRNA"
	/db_xref="taxon:6253"
	/sex="Male"
	/tissue_type="Intestine"
	/dev_stage="Adult"
	/lab_host="DH10B"
	/clone_lib="Ascaris suum male gut pAMP1 v2 Chiapelli McCarter"
	/notes=Vector: pAMP1 (Gibco); Site_1: NotI; Site_2: SalI; The library was constructed by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Dissected nematode tissues were provided by Dr. Alan Scott (ascott@jhph.edu) of the School of Public Health and Public Health at John Hopkins University in Baltimore, MD."

ORIGIN

Query Match	26.1%; Score 20.6; DB 3; Length 100;
Best Local Similarity	42.4%; Pred.No. 3.7e+04;
Matches	25; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

Qy 12 GAGACAGCGCGCUGGCCCUUAUUGUACUUCGGCGCUAUUGUCUCCUUC 70
||| ||| ||| ||| ||| : : : ||| : : ||| : : ||| : : ||| : : ||| : :

Dd 1 GAGCTCTGCGGCTCCAGCCAACTTACTGAAGCGTTTCGTGCCTACCATC 59
||| ||| ||| ||| ||| ||| : : : ||| : : ||| : : ||| : : ||| : :

RESULT 6

BF147704/c	85 bp mRNA linear EST 26-OCT-2000
LOCUS	us40a01.x1 Soares_NMEBA_branchial_arch Mus musculus cDNA clone IMAGE:3169512 3' similar to TR:Q15022 Q15022 ORF ; mRNA sequence.
DEFINITION	BF147704
ACCESSION	BF147704.1 GI:11029099
VERSION	EST.
KEYWORDS	Mus musculus (house mouse)
SOURCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
ORGANISM	1 (bases 1 to 85)
REFERENCE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ngicgap.
AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
TITLE	Other ESTs: us40a01.y1
JOURNAL	Contact: Robert Strausberg, Ph.D.
COMMENT	Email: cgapbs-r@mail.nih.gov cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

TITLE

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
image.lnl.gov/image/html/iresources.shtml

MG1:1064972

Trace considered overall poor quality
 Possible reversed clone: polyT not found
 High quality sequence stop: 1.

FEATURES

source
 Location/Qualifiers

```
1..85
/mol_type="mRNA"
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3169512"
/tissue_type="branchial arches"
/dev_stage="embryo, 10.5 dpc"
/lab_host="DH10B (phage resistant)"
/clone_lib="Soares NM8BA branchial arch"
/note="Vector: pT73D-PaCi; Site_1: NotI; Site_2: EcoRI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TGTTACCAATCTGAAGTGGAGCGCGCGCATGATTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
```

ORIGIN

```
Query Match      25.6%; Score 20.2; DB 7; Length 85;
Best Local Similarity 59.2%; Pred. No. 5e+04;
Matches 29; Conservative 2; Mismatches 18; Indels 0; Gaps 0;

QY 1 GGAGGGCGGGGAGAGACGAGCGGCGUCUGGCCCUUAAUUGUACUUCGG 49
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 51 GCGCGGGGAGGAGGAGCAGGACCGCATGCGGCTCAGAGCAGCGCGG 3
```

RESULT 7

```
AI616438/c
LOCUS      100 bp mRNA linear EST 21-APR-1999
DEFINITION zeh0074.seq.F Zebrafish Embryonic Heart cDNA Library Danio rerio
            cDNA 5', mRNA sequence.
ACCESSION  AI616438
VERSION     AI616438.1 GI:4625605
KEYWORDS   EST.
SOURCE      Danio rerio (zebrafish)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1 (bases 1 to 100)
AUTHORS     Ton, C., Mably, J.D., Dempsey, A.A., Hwang, D.M., Fishman, M.C. and
            Liew, C.C.
TITLE       Identification and Characterization of Expressed Sequence Tags from
            an Embryonic Zebrafish Heart cDNA Library
JOURNAL     Unpublished (1999)
COMMENT     Contact: Liew CC
            Brigham and Women's Hospital
            Harvard Medical School
            75 Francis St. Boston, MA 02115, USA
            Tel: 6177328915
            Fax: 6179750995
            Email: cliew@rics.bwh.harvard.edu
PCR PRIMERS
FORWARD: 5' GCGAAGCTCGAATTAACCTCACTAAAGGG 3'
BACKWARD: 5' CCAGTGATTTGTAATACGACTCACTATAGGGCG 3'
Seq primer: 5' GAATTAACCTCACTAAAGGG 3'.
```

FEATURES

source
 Location/Qualifiers

```
1..100
/organism="Danio rerio"
```

```
/mol_type="mRNA"
/db_xref="taxon:7955"
/dev_stage="embryonic day 3 post-fertilization"
/lab_host="E.coli XL1-Blue mrf"
/clone_lib="Zebrafish Embryonic Heart cDNA Library"
/note="Organ: heart; Vector: Lambda ZAP Express; Site_1:
EcoRI; Site_2: XhoI; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). cDNA was
synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI
adaptors were ligated, followed by digestion with XhoI,
for directional cloning into pre-digested lambda ZAP
Express vector."
```

ORIGIN

```
Query Match      25.6%; Score 20.2; DB 1; Length 100;
Best Local Similarity 45.2%; Pred. No. 5e+04;
Matches 33; Conservative 7; Mismatches 33; Indels 0; Gaps 0;

QY 1 GGAGGGCGGGGAGAGACGAGCGGCGUCUGGCCCUUAAUUGUACUUCGGCGCUAUUGU 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 97 GGGGCTCGGGGCTGCTCTCTGGGGAATCCTCTGAAGGCCCTTCGCCGGGGCGGCG 38
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 CUCUCUUUCGCC 73
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 37 CTCTCTTCCTCC 25
```

RESULT 8

```
CC183143/c
LOCUS      81 bp mRNA linear GSS 08-MAY-2003
DEFINITION XE629 BayGenomics Gene Trap Library pGTLxf Mus musculus cDNA, mRNA
            sequence.
ACCESSION  CC183143
VERSION     CC183143.1 GI:30427043
KEYWORDS   GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 81)
AUTHORS     BayGenomics.
TITLE       http://baygenomics.ucsf.edu/
JOURNAL     Unpublished (2001)
COMMENT     Contact: BayGenomics
            Bay Area Functional Genomics Consortium (BayGenomics)
            Email: info@baygenomics.ucsf.edu
            Sequence tag generated by 5' RACE of total RNA from gene trap ES
            cell line. ES cell lines harboring insertion mutation of target
            gene are available upon request from BayGenomics. Annotation
            information available from
            http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
            CELL_LINE&KEY=XE629
            Class: Gene Trap.
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FEATURES

source
 Location/Qualifiers

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1..81
/organism="Mus musculus"
/mol_type="mRNA"
/strains="129 ola"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGTLxf"
/note="Vector: pGTLxf"
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ORIGIN

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Query Match      25.3%; Score 20; DB 12; Length 81;
Best Local Similarity 32.7%; Pred. No. 5.8e+04;
Matches 17; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 28 UGGCCCCUUAUUGUACUUCGGCGCUUAAUUGUACUUCGCCACCUCC 79
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 67 TGAACCTTCTCTCTTTGGGGGCTGCTGTGTGTTCTCTCTCTCTTGC 16
```



```

RESULT 9
H55638/c
LOCUS
DEFINITION   CHR220577 Chromosome 22 exon Homo sapiens cDNA clone C22_783 5',
              mRNA sequence.
ACCESSION   H55638
VERSION     H55638.1  GI:1108504
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominoidea; Homo.
REFERENCE   1 (bases 1 to 88)
AUTHORS    Trofatter,J.A., Long,K.R., Murrell,J.R., Stotler,C.J., Gusella,J.F.
            and Buckler,A.J.
TITLE      An expression-independent catalog of genes from human chromosome 22
JOURNAL    Genome Res. 5 (3), 214-224 (1995)
PUBMED    8593609
COMMENT     Contact: Buckler AJ
            Molecular Neurogenetics Unit
            Massachusetts General Hospital
            Building 149, 13th St., Charlestown MA 02129
            Tel: 6177249616
            Fax: 6177265736
            Email: buckler@helix.mgh.harvard.edu
            Seq primer: T3.

FEATURES             Location/Qualifiers
     source           1..88
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="C22_783"
                     /lab_host="E. coli DH5a"
                     /clone_lib="Chromosome 22 exon"
                     /notes="Vector: pBluescriptKS+; Site 1: Sal I; Site 2:
                     Bam HI (destroyed); Exons were isolated from human
                     chromosome 22 specific cosmids using a modification of
                     the method of exon amplification (Proc. Natl. Acad. Sci.
                     USA 88:4005-4009, 1991). Amplified exons were digested
                     with Sal I and Bgl II and subsequently cloned into
                     pBluescriptKS+ at the Sal I and Bam HI sites."

ORIGIN
Query Match      25.3%; Score 20; DB 10; Length 88;
Best Local Similarity 44.4%; Pred. No. 5.8e+04;
Matches 16; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Qy 28 UGCGCCCUUAUUGUACUUCGGCGUCGUUUGUCUC 63
      :|||:||||:||||:||||:||||:||||:
Db 70 TGTGACCCCTAATTGTTCTTCTGCTGCTCTAATAGTCTC 35

RESULT 10
CT351516/c
LOCUS
DEFINITION   Sus scrofa genomic clone CH242-438014, genomic survey sequence.
ACCESSION   CT351516
VERSION     CT351516.1  GI:79928188
KEYWORDS    GSS.
SOURCE      Sus scrofa (pig)
ORGANISM    Sus scrofa
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
             Sus.
REFERENCE   1 (bases 1 to 78)
AUTHORS    Humphray,S.J., Plumb,R.W. and Durham,J.L.
TITLE      Direct Submission
JOURNAL    Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished

COMMENT     This sequence was generated from the T7 end of BAC 438014. 438014
            is part of the CHORI-242 BAC Library created by P. de Jong. Further
            details: http://www.sanger.ac.uk/projects/S_scrofa/.

FEATURES             Location/Qualifiers
     source           1..78
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9823"
                     /clone="CH242-438014"
                     /tissue_type="White blood cells"
                     /note="Vector pTARBAC1.3_BamHI
                     sex female"

ORIGIN
Query Match      25.1%; Score 19.8; DB 14; Length 78;
Best Local Similarity 38.3%; Pred. No. 6.8e+04;
Matches 18; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Qy 33 CCUUAUUGUACUUCGGCGUCGUUUGUCUCUCCUCCUCCUCCUCC 79
      |||:||||:||||:||||:||||:||||:
Db 47 CATGAATGATTTAGAGCTGCTTTTGCGACTTCTTTAGGCGCGCTCC 1

RESULT 11
CW115558/c
LOCUS
DEFINITION   104 490 11106626 116 34591.001 Sorghum methylation filtered library
              (LibID: 104) Sorghum bicolor genomic clone 11106626, genomic survey
              sequence.
ACCESSION   CW115558
VERSION     CW115558.1  GI:54808105
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
ORGANISM    Sorghum bicolor
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
             clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1 (bases 1 to 83)
AUTHORS    Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A., Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddelloh,J.A. and
            Martienssen,R.A.
TITLE      Sorghum genome sequencing by methylation filtration
JOURNAL    PLOS Biol. 3 (1), e13 (2005)
PUBMED    15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 490 row: o column: 02
            Seq primer: T3 Reverse
            Class: methylation filtered
            High quality sequence stop: 83.

FEATURES             Location/Qualifiers
     source           1..83
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="Atx823"
                     /db_xref="taxon:4558"
                     /clone="11106626"
                     /clone_lib="Sorghum methylation filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation filtered library."

ORIGIN

```

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Query Match      25.1%; Score 19.8; DB 13; Length 83;
Best Local Similarity 44.4%; Pred. No. 6.8e+04;
Matches 28; Conservative 8; Mismatches 27; Indels 0; Gaps 0;

QY 2 GAGGGCGGGGAGAGACGAGCGGCGUCUGGCCCCUUAUUGUACUUCGGCGGCGUUAUUGUC 61
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 67 GAAGACGGCCCTCATCGGGCCCAACCTGGACCCCTAAATAGGAGAGCGCGCTCGTCAGGTT 8
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 62 UCU 64
   :|:
Db 7 TCT 5

RESULT 12
CWL15559
LOCUS
DEFINITION
CWL15559 83 bp DNA linear GSS 29-OCT-2004
104_490_11106626_148_34587_001 Sorghum methylation filtered library
(LiBID: 104) Sorghum bicolor genomic clone 11106626, genomic survey
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sorghum bicolor (sorghum)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 83)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holeman,H., Roe,B.A., Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddleloh,J.A. and
Martensen,R.A.
Sorghum genome sequencing by methylation filtration
PLOS Biol. 3 (1), e13 (2005)
15660154
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 490 row: 0 column: 02
Seq primer: Sfor Forward
Class: methylation filtered
High quality sequence stop: 83.
Location/Qualifiers
1. 83
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
/clone="11106626"
/clone_lib="Sorghum methylation filtered library (LiBID:
104)"
/notes="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to 5
kb fraction, ligated into HincII-digested pBCSK(-) vector
and electroporated into E. coli cells. This is a
methylation filtered library."

ORIGIN
source
Query Match      25.1%; Score 19.8; DB 13; Length 83;
Best Local Similarity 44.4%; Pred. No. 6.8e+04;
Matches 28; Conservative 8; Mismatches 27; Indels 0; Gaps 0;

QY 2 GAGGGCGGGGAGAGACGAGCGGCGUCUGGCCCCUUAUUGUACUUCGGCGGCGUUAUUGUC 61
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 15 GAAGACGGCCCTCATCGGGCCCAACCTGGACCCCTAAATAGGAGAGCGCGCTCGTCAGGTT 74
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QY 62 UCU 64
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```

Db 75 TCT 77

RESULT 13
CWL20424
LOCUS
DEFINITION
CWL20424 71 bp mRNA linear GSS 28-SEP-2004
GC0686 TIGEM gene trap library Mus musculus cDNA clone A011.G4,
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 71)
Cobellis,G., Nicolois,M., Di Giorgio,F.P., Iovino,N., Zollo,M.,
Barbaisi,M., Sardiello,M.,
Ballabio,A. and Cortese,R.
Tagging genes with cassette-exchange sites
Nucleic Acids Res. 33 (4), e44 (2005)
15741177
Contact: TIGEM
107
TIGEM
Via P. Castellino, 111, 80131 NAPOLI, ITALY
Tel: +390816132205
Fax: +390815790919
Email: cobellis@tigem.it
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from TIGEM. Annotation information
available from TIGEM
Class: Gene trap.
Location/Qualifiers
1. 71
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Ola"
/db_xref="taxon:10090"
/clone="A011.G4"
/sex="male"
/cell_type="Embryonic stem cell"
/cell_line="E14"
/clone_lib="TIGEM gene trap library"
/notes="Vector: pFLIPl"

ORIGIN
source
Query Match      24.8%; Score 19.6; DB 13; Length 71;
Best Local Similarity 52.0%; Pred. No. 7.8e+04;
Matches 26; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 GGAGCGCGGGGAGAGACGAGCGGCGUCUGGCCCCUUAUUGUACUUCGGG 50
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 GGGGGGGGGGAAAAACGGGGGGGGCCCCCCCCCTTTTATACAGGGGG 50
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 14
CWL21192/c
LOCUS
DEFINITION
CWL21192 84 bp mRNA linear EST 19-SEP-2005
PCRS50390_2 Hematopoietic stem cells Mus musculus cDNA, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 84)
Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and

```

TITLE Lemischka, I.R.
JOURNAL Diversification of Stem Cell Molecular Repertoire by Alternative
COMMENT Splicing
Proc. Natl. Acad. Sci. U.S.A. (2005) In press
Contact: Pritsker M
Lab of Ihor Lemischka, Department of Molecular Biology
Princeton University
Princeton, NJ 08544, USA
Tel: 609 258 5657
Fax: 609 258 1704
Email: pritaker@molbio.princeton.edu.

FEATURES

source

1. .84
Location/Qualifiers
/organism="Mus musculus"
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/db_xref="taxon:10090"
/tissue_type="Hematopoietic stem cells"
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/clone_lib="Hematopoietic stem cells"
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hematopoietic stem cells"

ORIGIN

Query Match 24.8%; Score 19.6; DB 10; Length 84;
Best Local Similarity 36.2%; Pred. No. 8e+04;
Matches 21; Conservative 13; Mismatches 24; Indels 0; Gaps 0;
QY 21 GCGGCGUCUGCCUUAUUGUACUUGCGGCGUUAUUGUCUUCUUGCGCACCCUC 78
Db 79 GCGGGCTTGGCCCCCTTATTGGGTGGTCCCTTTTGGGTCTCTGAGCTCCGTC 22

RESULT 15

AJ649396

LOCUS

AJ649396 CSEQRAN19 Sus scrofa cDNA clone C0003272_F23, mRNA
85 bp mRNA linear EST 07-JUL-2004

DEFINITION

sequence.

ACCESSION

AJ649396

VERSION

AJ649396.1

GI:49326241

KEYWORDS

EST.

SOURCE

Sus scrofa (pig)

ORGANISM

Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE

1 (bases 1 to 85)

Anderson, S.I., Finlayson, H.A. and Archibald, A.L.

Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle

Unpublished (2004)

Contact: Anderson SI

Genomics and Bioinformatics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector: pBlueScriptII (KS) R. Site1: EcoRI
R. Site2: NotI 5' Seg Primer M13F Normalised library constructed
from pooled ovaries. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.ark-genomics.org.

EH25 9PS, www.ark-genomics.org.

Location/Qualifiers

1. .85

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="C0003272_F23"

/tissue_type="ovary"

/clone_lib="CSEQRAN19"

/note="Vector: pBlueScriptII (KS+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing; Normalised library
constructed from pooled ovaries"

ORIGIN

Query Match 24.8%; Score 19.6; DB 1; Length 85;
Best Local Similarity 42.0%; Pred. No. 8e+04;
Matches 21; Conservative 10; Mismatches 19; Indels 0; Gaps 0;
QY 16 GACGAGCGGCGUCUGGCCCCCUUAUUGUACUUCGCGGCGUUAUUGUCUCUC 65
Db 8 GTGCGGAGCGGCTGGCGCTTCCTCCTCGCGAGTGAATGGTCTCTC 57

Search completed: October 16, 2006, 16:16:48

Job time : 4331 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:28:14 ; Search time 110 Seconds
(without alignments)
1343.796 Million cell updates/sec

Title: US-10-604-726A-5135
Perfect score: 79
Sequence: 1 ggaagcggggagagacga.....ucucuccuuccaccucc 79

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 1560966

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1 COMB.seq: *
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5 COMB.seq: *
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB.seq: *
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B COMB.seq: *
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq: *
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H COMB.seq: *
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS COMB.seq: *
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB.seq: *
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq: *
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20.4	25.8	86	5	US-09-543-679A-1233
2	20	25.3	93	3	US-09-621-976-18431
3	19.8	25.1	63	2	US-08-014-723-12
4	19.8	25.1	63	2	US-08-110-011A-12
5	19.4	24.6	97	3	US-08-952-793-288
6	19.4	24.6	97	3	US-09-849-928-288
7	19.4	24.6	97	7	PCT-US96-09455A-288
8	19.2	24.3	51	3	US-09-513-999C-14603
9	19	24.1	65	2	US-08-014-723-11
10	19	24.1	65	2	US-08-110-011A-11
11	18.8	23.8	39	3	US-09-367-791A-19
12	18.8	23.8	54	3	US-08-444-818-753
13	18.8	23.8	79	3	US-08-687-421-415
14	18.4	23.3	62	3	US-08-965-762-27
15	18.4	23.3	62	3	US-09-911-927-27
16	18.4	23.3	62	3	US-09-911-882-27
17	18.4	23.3	62	3	US-09-911-888-27
18	18.4	23.3	65	3	US-09-513-999C-15806
19	18.2	23.0	65	2	US-08-086-410-28
20	18	22.8	42	3	US-09-475-947A-86
21	18	22.8	78	2	US-08-090-193-16
22	18	22.8	78	2	US-08-488-031-16
23	18	22.8	78	2	US-08-486-569-16

C 24	18	22.8	78	2	US-08-488-027-16	Sequence 16, Appl
C 25	18	22.8	78	2	US-08-090-192-16	Sequence 16, Appl
C 26	18	22.8	78	2	US-08-482-663-16	Sequence 16, Appl
C 27	18	22.8	78	3	US-08-482-658-16	Sequence 16, Appl
C 28	18	22.8	78	3	US-08-470-349-16	Sequence 16, Appl
C 29	18	22.8	78	3	US-08-475-610-16	Sequence 16, Appl
C 30	18	22.8	78	7	PCT-US92-00277-16	Sequence 16, Appl
C 31	18	22.8	78	7	PCT-US92-00278-16	Sequence 16, Appl
C 32	17.8	22.5	77	5	US-09-844-508-25	Sequence 25, Appl
C 33	17.8	22.5	87	3	US-09-873-075A-5	Sequence 5, Appl
C 34	17.6	22.3	87	4	US-09-393-803-68	Sequence 68, Appl
C 35	17.6	22.3	50	3	US-10-131-827-847	Sequence 847, Appl
C 36	17.6	22.3	50	5	US-10-131-831-847	Sequence 847, Appl
C 37	17.6	22.3	59	2	US-08-790-963-53	Sequence 53, Appl
C 38	17.6	22.3	59	3	US-09-371-774-53	Sequence 53, Appl
C 39	17.6	22.3	59	3	US-09-875-082-53	Sequence 13, Appl
C 40	17.4	22.0	72	2	US-08-433-126A-13	Sequence 13, Appl
C 41	17.4	22.0	72	2	US-08-433-124A-13	Sequence 13, Appl
C 42	17.4	22.0	72	3	US-08-976-413A-13	Sequence 13, Appl
C 43	17.4	22.0	72	7	PCT-US96-06059-13	Sequence 13, Appl
C 44	17.4	22.0	91	3	US-09-513-999C-15862	Sequence 15862, A
C 45	17.2	21.8	54	3	US-09-621-976-13448	Sequence 13448, A

ALIGNMENTS

RESULT 1
US-09-543-679A-1233
; Sequence 1233, Application US/09543679A
; Patent No. 7034007
; GENERAL INFORMATION:
; APPLICANT: NTC, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
; COMPOSITIONS, KIT & METHOD FOR TREATMENT
; OF AIRWAY DISORDERS ASSOCIATED WITH
; BRONCHOCONSTRICTION, LUNG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: N/A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/543,679A
; FILING DATE: 13-Apr-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/127,958
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 1233:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1233:

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US-09-543-679A-1233
Query Match      25.8%; Score 20.4; DB 5; Length 86;
Best Local Similarity 38.6%; Pred. No. 3.6e+02;
Matches 27; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

Qy 4 GGGGGGGGAGACGAGCGGCGUCUGGCCCUAAUUGUACUUGCGGCGUUAUUGUCUC 63
Db 1 GGGGGGCGBCBGTGGGCGCCCBHGGCCCTCTCGTTCBCTTCTGCGCBGGBGTTCBT 60

Qy 64 UCCUUGGCC 73
Db 61 CCCCBTBTGC 70

RESULT 2
US-09-621-976-18431/c
Sequence 18431, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 18431
LENGTH: 93
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 63..64,83
OTHER INFORMATION: n=a, g, c or t
US-09-621-976-18431

Query Match      25.3%; Score 20; DB 3; Length 93;
Best Local Similarity 63.9%; Pred. No. 5.2e+02;
Matches 23; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 5 GGGGGGAGACGAGCGGCGUCUGGCCCUAAU 40
Db 58 GGGGGGCGGCGACGAGCGGCTCAGGCCCTCGAGT 23

RESULT 3
US-08-014-723-12/c
Sequence 12, Application US/08014723
Patent No. 5273962
GENERAL INFORMATION:
APPLICANT: Doi, Takeshi
APPLICANT: Iwasaki, Akio
APPLICANT: Saino, Yushi
APPLICANT: Kimura, Shigeru
APPLICANT: Ohkuchi, Masao
TITLE OF INVENTION: Thrombin-Binding Substance and Process
TITLE OF INVENTION: For Preparing the Same
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,011A
FILING DATE: 23-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5354664man F.
REGISTRATION/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-073-0 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-014-723-12
Query Match      25.1%; Score 19.8; DB 2; Length 63;
Best Local Similarity 59.0%; Pred. No. 5.6e+02;
Matches 23; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Qy 3 AGGGGGGAGACGAGCGGCGUCUGGCCCUAAUUG 41
Db 40 AGTGCACGACGAGCGGCGCTGTGGCGACTGACTCG 2

RESULT 4
US-08-110-011A-12/c
Sequence 12, Application US/08110011A
Patent No. 5354664
GENERAL INFORMATION:
APPLICANT: Doi, Takeshi
APPLICANT: Iwasaki, Akio
APPLICANT: Saino, Yushi
APPLICANT: Kimura, Shigeru
APPLICANT: Ohkuchi, Masao
TITLE OF INVENTION: Thrombin-Binding Substance and Process
TITLE OF INVENTION: For Preparing the Same
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
ADDRESSEE: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,011A
FILING DATE: 23-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5354664man F.
REGISTRATION/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-073-0 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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QY 19 GAGCGCUCUGGCCCCUUAUUGUACUCGGGCGUCGUAUUGUCUCUCCUUGCCACCCUC 78
Db 90 GTGAGCCTCTGTGCGAATCTTACTACTTCTGCTTTGTGTTTGTGTTGCGTGCCCTT 31

QY 79 C 79
Db 30 C 30

RESULT 7
PCT-US96-09455A-288/c
; Sequence 288, Application PC/TUS9609455A
; GENERAL INFORMATION:
; APPLICANT: PARMA, et al.
; TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID
; TITLE OF INVENTION: LIGANDS TO LECTINS
; NUMBER OF SEQUENCES: 390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09455A
; FILING DATE: 05 JUNE 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,724
; FILING DATE: 07-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/472,256
; FILING DATE: 07-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/472,255
; FILING DATE: 07-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,829
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX40C/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 288:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; FEATURE:
; OTHER INFORMATION: All C's are 2'-NH2 cytosine
; FEATURE:
; OTHER INFORMATION: All U's are 2'-NH2 uracil
PCT-US96-09455A-288

Query Match 24.6%; Score 19.4; DB 7; Length 97;
Best Local Similarity 31.1%; Pred. No. 8.9e+02;
Matches 19; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
QY 19 GAGCGCUCUGGCCCCUUAUUGUACUCGGGCGUCGUAUUGUCUCUCCUUGCCACCCUC 78
Db 90 GTGAGCCTCTGTGCGAATCTTACTACTTCTGCTTTGTGTTTGTGTTGCGTGCCCTT 31

QY 79 C 79
Db 30 C 30

RESULT 8
US-09-513-999C-14603/c
; Sequence 14603, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 14603
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-14603

Query Match 24.3%; Score 19.2; DB 3; Length 51;
Best Local Similarity 60.0%; Pred. No. 8.9e+02;
Matches 24; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
QY 1 GGAGGGCGGGGAGAGACGAGCGGCGUCUGGCCCCUUAUU 40
Db 47 GGGCGGCGGGCGGCGAGCAGCGGCTCAGGCCCCGTCGACT 8

RESULT 9
US-08-014-723-11
; Sequence 11, Application US/08014723
; Patent No. 5273962
; GENERAL INFORMATION:
; APPLICANT: Doi, Takeshi
; APPLICANT: Iwasaki, Akio
; APPLICANT: Saino, Yushi
; APPLICANT: Kimura, Shigeru
; APPLICANT: Ohkuchi, Masao
; TITLE OF INVENTION: Thrombin-Binding Substance and Process
; TITLE OF INVENTION: For Preparing the Same
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,723
; FILING DATE: 19930208
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5273962man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 80-071-0 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)413-3000


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DB      30 AGGTCAGCAGCGGCCACCGCTCTGGCGACTGA 64

RESULT 11
US-09-367-791A-19
; Sequence 19, Application US/09367791A
; Patent No. 6573071
; GENERAL INFORMATION:
; APPLICANT: Himmelspach, Michele
; Schlokat, Uwe
; Dörner, Friedrich
; Fisch, Andreas
; Eibl, Johann
TITLE OF INVENTION: Factor X Analogues With
; a Modified Protease Cleavage Site
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/367,791A
; FILING DATE: 12-No. 6573071-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AT A 335/97
; FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/00045
; FILING DATE: 27-FEB-1998
ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,471
REFERENCE/DOCKET NUMBER: 20695D-000700U5
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-367-791A-19

Query Match 23.8%; Score 18.8; DB 3; Length 33
Best Local Similarity 44.7%; Pred.No.1.2e+03;
Matches 17; Conservative 9; Mismatches 12; Indels

QY      33 CCUAUAUGUACUUCGGGCUCGUUUGUCUCCUUCUUC 70
|| ||| :|||:|||:|||:|||:|||:|
DB      2 CCAGAATCATTTCTGTGCTCGTGTTCGCCCTCTC 39

RESULT 12
US-08-444-818-753/c
; Sequence 753, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANB Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777

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RESULT 15

US-09-911-927-27
; Sequence 27, Application US/09911927
; Patent No. 6461826
; GENERAL INFORMATION:
; APPLICANT: Koltin, Yigal
; APPLICANT: Gavrilas, Victoria
; TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
; FILE REFERENCE: 06286-062003
; CURRENT APPLICATION NUMBER: US/09/911,927
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 08/965,762
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 62
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for PCR
US-09-911-927-27

Query Match 23.3%; Score 18.4; DB 3; Length 62;
Best Local Similarity 38.5%; Pred. No. 1.9e+03;
Matches 20; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Qy 27 CUGGCCCUUAUUGUACUUGGGCUGGUAGUUGUCUCCUUGCGCACCCUC 78
Db 8 CCGCGCCCATCATGCAAGATCCTGTATGATGACATTCCTTTGGCCTCCTC 59

Search completed: October 16, 2006, 14:34:12
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Copyright (c) 1993 - 2006 Bioceleration Ltd.
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Title: US-10-604-726A-5135
Perfect score: 79
Sequence: 1 ggaagggcgggagagacga.....ucucuccuuccaccucc 79
Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0
Searched: 18932170 seqs, 6143817638 residues
Total number of hits satisfying chosen parameters: 24414840
Minimum DB seq length: 0
Maximum DB seq length: 100
Post-processing: Minimum Match 0%
Maximum Match 100%
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Database : Published Applications_NA_Main:*

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
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8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
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13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	27	34.2	67	11	US-10-310-914A-16611
C 2	23	29.1	87	3	Sequence 16611, A
C 3	19.4	24.6	97	3	Sequence 4883, Ap
C 4	19.4	24.6	97	6	Sequence 288, App
C 5	19.4	24.6	97	6	Sequence 288, App
C 6	19.4	24.6	97	8	Sequence 288, App
C 7	19.2	24.3	80	8	Sequence 288, App
C 8	19.2	24.3	80	8	Sequence 6, Appli
C 9	19.2	24.3	87	3	Sequence 1387, Ap
C 10	19	24.1	86	16	Sequence 22, Appl
C 11	18.8	23.8	24	11	Sequence 37212, A
C 12	18.8	23.8	39	7	Sequence 19, Appl
C 13	18.8	23.8	72	3	Sequence 15, Appl
C 14	18.8	23.8	72	9	Sequence 15, Appl
C 15	18.8	23.8	72	13	Sequence 15, Appl
C 16	18.6	23.5	55	10	Sequence 3, Appli
C 17	18.6	23.5	65	3	Sequence 3993, Ap

C 18	18.6	23.5	80	8	US-10-384-245-10
C 19	18.6	23.5	94	3	US-09-864-761-24937
C 20	18.6	23.5	99	11	US-10-932-182A-173876
C 21	18.4	23.3	50	16	Sequence 173876, A
C 22	18.4	23.3	62	3	Sequence 47265, A
C 23	18.4	23.3	62	3	US-09-911-888-27
C 24	18.4	23.3	62	3	US-09-911-927-27
C 25	18.4	23.3	90	8	US-10-296-734-485
C 26	18.4	23.3	94	11	US-10-310-914A-15206
C 27	18.2	23.0	50	16	US-11-175-859-73819
C 28	18.2	23.0	60	3	US-09-908-975-10452
C 29	18.2	23.0	63	9	US-10-819-095-9
C 30	18.2	23.0	65	3	US-09-908-975-931
C 31	18	22.8	90	8	US-10-296-734-314
C 32	18	22.8	80	8	US-10-384-245-343
C 33	17.8	22.5	24	11	US-10-310-914A-914124
C 34	17.8	22.5	77	3	US-09-844-508-25
C 35	17.8	22.5	77	6	US-10-084-826-25
C 36	17.8	22.5	87	3	US-09-873-075A-5
C 37	17.8	22.5	87	16	US-11-115-425-68
C 38	17.8	22.5	100	3	US-09-728-445-363
C 39	17.8	22.5	100	10	US-10-964-549-363
C 40	17.6	22.3	25	13	US-11-036-317-296412
C 41	17.6	22.3	25	13	US-11-036-317-372387
C 42	17.6	22.3	25	13	US-11-036-317-976170
C 43	17.6	22.3	50	7	US-10-131-827-847
C 44	17.6	22.3	50	16	US-11-175-859-8102
C 45	17.6	22.3	50	16	US-11-175-859-29840

ALIGNMENTS

RESULT 1
US-10-310-914A-16611/c
; Sequence 16611, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuvzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16611
; LENGTH: 67
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-16611

Query Match	34.2%	Score 27;	DB 11;	Length 67;
Best Local Similarity	80.0%;	Pred. No. 6.8;		
Matches	28;	Conservative	2;	Mismatches 5; Indels 0; Gaps 0;
Qy	1	GGAGGGCGGGGAGAGACGAGCGGCGUCUGGCCCCU	35	
Db	67	GGAGGGCTGGGAGAGAGAGAGCCCTGGCCCT	33	
RESULT 2				
US-09-294-093B-4883/c				
; Sequence 4883, Application US/09294093B				
; Patent No. US20010051335A1				
; GENERAL INFORMATION:				
; APPLICANT: Ialguidi, Raghunath, V.				
; APPLICANT: Ito, Laura, Y.				
; APPLICANT: Sherman, Bradley, K.				
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL				
; FILE REFERENCE: PL-0009 US				
; CURRENT APPLICATION NUMBER: US/09/294,093B				

; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 4883
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700355274H1
; NAME/KEY: unsure
; LOCATION: 32, 35, 37, 42-43, 52, 57, 69, 79, 81
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-4883

Query Match 29.1%; Score 23; DB 3; Length 87;
Best Local Similarity 43.7%; Pred. No. 2.2e+02;
Matches 31; Conservative 7; Mismatches 33; Indels 0; Gaps 0;

QY 9 GGGGAGAGACGAGCGGCUUGGCCCCUUAUUGUACUUCGGGCUUGUUGUCUUCUCCUU 68
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Db 73 GGGGAGAGTCGGTGGNAGTTCCTGCAANNCTATNTNGANCTCGCTCGACCTCGCCGA 14
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QY 69 UCGCCACCUCC 79
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Db 13 ACGTCAGCTCC 3

RESULT 3
US-09-849-928-288/c
; Sequence 288, Application US/0984928
; Publication No. US20030059769A1
; GENERAL INFORMATION:
; APPLICANT: PARMA, et al.
; TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
; NUMBER OF SEQUENCES: 390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/849,928
; FILING DATE: 04-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/952,793
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/479,724
; FILING DATE: 07-JUNE-1995
; APPLICATION NUMBER: 08/472,256
; FILING DATE: 07-JUNE-1995
; APPLICATION NUMBER: 08/472,255
; FILING DATE: 07-JUNE-1995
; APPLICATION NUMBER: 08/477,829
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX40C/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433

; INFORMATION FOR SEQ ID NO: 288:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; FEATURE:
; OTHER INFORMATION: All C's are 2'-NH2 cytosine
; FEATURE:
; OTHER INFORMATION: All U's are 2'-NH2 uracil
; SEQUENCE DESCRIPTION: SEQ ID NO: 288:
US-09-849-928-288

Query Match 24.6%; Score 19.4; DB 3; Length 97;
Best Local Similarity 31.1%; Pred. No. 5.1e+03;
Matches 19; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 19 GAGCGGCUUGGCCCCUUAUUGUACUUCGGGCUUGUUGUCUUCUCCUUGCCACCUCC 78
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 90 GTGAGCCCTCTGCGAATCTTACTTCTGCTTGTGTTTCTTCTTGTGCTGCTT 31
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 79 C 79
|
Db 30 C 30

RESULT 4
US-10-066-960-288/c
; Sequence 288, Application US/10066960
; Publication No. US20030049644A1
; GENERAL INFORMATION:
; APPLICANT: PARMA, et al.
; TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
; NUMBER OF SEQUENCES: 390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/066,960
; FILING DATE: 04-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/952,793
; FILING DATE: 1999-DEC-03
; APPLICATION NUMBER: PCT/US96/09455
; FILING DATE: 05-JUNE-1995
; APPLICATION NUMBER: 08/479,724
; FILING DATE: 07-JUNE-1995
; APPLICATION NUMBER: 08/472,256
; FILING DATE: 07-JUNE-1995
; APPLICATION NUMBER: 08/472,255
; FILING DATE: 07-JUNE-1995
; APPLICATION NUMBER: 08/477,829
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX40C/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 288:

SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-NH2 cytosine
FEATURE:
OTHER INFORMATION: All U's are 2'-NH2 uracil
SEQUENCE DESCRIPTION: SEQ ID NO: 288;
US-10-066-960-288

Query Match 24.6%; Score 19.4; DB 6; Length 97;
Best Local Similarity 31.1%; Pred. No. 5.1e+03;
Matches 19; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
QY 19 GAGCGCUCUGCCCUUAUUGUACUUGCGGCGUUAUUGUCUCCUUGCGCACCCUC 78
DB 90 GTGAGCCTCTCTCGAATCTTACTTCTGCTTTGTTGTTTCTGCGTGCCTT 31
QY 79 C 79
DB 30 C 30

RESULT 5
US-10-409-627-288/c
Sequence 288, Application US/10409627
Publication No. US20040043923A1
GENERAL INFORMATION:

APPLICANT: PARMA, et al.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TO LECTINS

NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/409,627
FILING DATE: 07-Apr-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/952,793
FILING DATE: 20-NOVEMBER-1997
APPLICATION NUMBER: PCT/US96/09455
FILING DATE: 05-JUNE-1995
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995

ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 288:
SEQUENCE CHARACTERISTICS:

LENGTH: 97 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-NH2 cytosine
FEATURE:
OTHER INFORMATION: All U's are 2'-NH2 uracil
SEQUENCE DESCRIPTION: SEQ ID NO: 288;
US-10-409-627-288

Query Match 24.6%; Score 19.4; DB 8; Length 97;
Best Local Similarity 31.1%; Pred. No. 5.1e+03;
Matches 19; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
QY 19 GAGCGCUCUGCCCUUAUUGUACUUGCGGCGUUAUUGUCUCCUUGCGCACCCUC 78
DB 90 GTGAGCCTCTCTCGAATCTTACTTCTGCTTTGTTGTTTCTGCGTGCCTT 31
QY 79 C 79
DB 30 C 30

RESULT 6
US-10-705-300-288/c
Sequence 288, Application US/10705300
Publication No. US20040072234A1
GENERAL INFORMATION:

APPLICANT: PARMA, et al.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TO LECTINS

NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/705,300
FILING DATE: 10-NOV-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/952,793
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: PCT/US96/09455
FILING DATE: 05-JUNE-1995
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995

ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 288:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; FEATURE:
; OTHER INFORMATION: All C's are 2'-NH2 cytosine
; FEATURE:
; OTHER INFORMATION: All U's are 2'-NH2 uracil
; SEQUENCE DESCRIPTION: SEQ ID NO: 288:
US-10-705-300-288

Query Match          24.6%; Score 19.4; DB 8; Length 97;
Best Local Similarity 31.1%; Pred. No. 5.1e+03;
Matches 19; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 19 GACGGCGUCUGGCCCCUAAUUGUACUUCGGGCGUCGUUUGUCUCCUUUGCCCAACUC 78
Db 90 GTGAGCTCTGTCGCAATCTTACTACTTCTGCTTGTGTTTGTTCCTTGCGTGCCTT 31
QY 79 C 79
Db 30 C 30

RESULT 7
US-10-448-250-6
; Sequence 6, Application US/10448250
; Publication No. US20040018530A1
; GENERAL INFORMATION:
; APPLICANT: Bowser, Michael T
; APPLICANT: Mendonsa, Shaun D
; TITLE OF INVENTION: IN VITRO EVOLUTION OF FUNCTIONAL RNA AND DNA USING
; TITLE OF INVENTION: ELECTROPHORETIC SELECTION
; FILE REFERENCE: 110.01870101
; CURRENT APPLICATION NUMBER: US/10/448,250
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/384,709
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/470,750
; PRIOR FILING DATE: 2003-05-15
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 80
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: aptamer
US-10-448-250-6

Query Match          24.3%; Score 19.2; DB 8; Length 80;
Best Local Similarity 35.9%; Pred. No. 5.9e+03;
Matches 23; Conservative 13; Mismatches 28; Indels 0; Gaps 0;

QY 6 GCGGGGAGAGACGAGCGGCGUCUUGGCCCCUAAUUGUACUUCGGGCGUCGUUUGUCUCUC 65
Db 2 GCAGCAGAGGTCAGATGTTGTACCGTTATTTGTGCTCAGCATCCCCGGGTAC 61
QY 66 CUU 69
Db 62 CTAT 65

RESULT 8
US-09-983-965-1387
; Sequence 1387, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Rao, Nengping
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
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; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 1387
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 23-LIB2809-008-Q1-E1-F3
US-09-983-965-1387

Query Match          24.3%; Score 19.2; DB 3; Length 87;
Best Local Similarity 37.5%; Pred. No. 5.9e+03;
Matches 15; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 31 CCCUUAUUGUACUUCGGGCGUCGUUUGUCUUCUUCUUC 70
Db 39 CCTCTTAATCTATATCTTACTCCAATTCACCTCCCTCTC 78

RESULT 9
US-11-106-909-22
; Sequence 22, Application US/11106909
; Publication No. US20060029950A1
; GENERAL INFORMATION:
; APPLICANT: WHITTEN, Jeffrey P.
; APPLICANT: SCHWABER, Michael
; APPLICANT: SIDDIQUI-JAIN, Adam
; APPLICANT: MORAN, Terence
; TITLE OF INVENTION: SUBSTITUTED QUINOBENZOXAZINE ANALOGS AND
; TITLE OF INVENTION: METHODS OF USING THEREOF
; FILE REFERENCE: 532232001121
; CURRENT APPLICATION NUMBER: US/11/106,909
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/903,975
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US 10/821,243
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/461,271
; PRIOR FILING DATE: 2004-07-03
; PRIOR APPLICATION NUMBER: US 60/463,171
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 60/519,535
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: US 60/532,727
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 86
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-106-909-22

Query Match          24.1%; Score 19; DB 16; Length 86;
Best Local Similarity 42.4%; Pred. No. 7.1e+03;
Matches 25; Conservative 9; Mismatches 25; Indels 0; Gaps 0;

QY 4 GGGCGGGGAGAGACGAGCGGCGUCUUGGCCCCUAAUUGUACUUCGGGCGUCGUUUGUCU 62
Db 9 GGGCGGGGCGGGGCGGCGGCTTAGCGACACGCAATTTCTATAGTGCATTAGCT 67

RESULT 10
US-11-228-636-22
; Sequence 22, Application US/11228636
; Publication No. US20060074089A1
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; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 72
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide containing S. cerevisiae DNA
US-09-918-740-15

Query Match      23.8%; Score 18.8; DB 3; Length 72;
Best Local Similarity 28.3%; Pred. No. 8.2e+03;
Matches 13; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

QY 33 CCUUAUUGUACUUCGGGCGUGUAUUGUCUCUCCUUUGCCACCUC 78
Db 72 CCTTAATTGTTCTTCATCAATAATCCTTTTCTCTGTGGGAATC 27

Search completed: October 16, 2006, 14:49:04
Job time : 883 secs
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RESULT 14
US-10-835-516-15/c
; Sequence 15, Application US/10835516
; Publication No. US20040194162A1
; GENERAL INFORMATION:
; APPLICANT: Hahn, Frederick
; TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathways
; FILE REFERENCE: KAS-103XC1
; CURRENT APPLICATION NUMBER: US/10/835,516
; CURRENT FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: US/09/918,740
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/221,703
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 72
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide containing S. cerevisiae DNA
US-10-835-516-15
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Query Match      23.8%; Score 18.8; DB 9; Length 72;
Best Local Similarity 28.3%; Pred. No. 8.2e+03;
Matches 13; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

QY 33 CCUUAUUGUACUUCGGGCGUGUAUUGUCUCUCCUUUGCCACCUC 78
Db 72 CCTTAATTGTTCTTCATCAATAATCCTTTTCTCTGTGGGAATC 27
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RESULT 15
US-11-053-541-15/c
; Sequence 15, Application US/11053541
; Publication No. US20050241017A1
; GENERAL INFORMATION:
; APPLICANT: Hahn, Frederick
; TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathways
; FILE REFERENCE: KAS-103XC1
; CURRENT APPLICATION NUMBER: US/11/053,541
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US/09/918,740
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/221,703
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:34:29 ; Search time 139 Seconds
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Title: US-10-604-726A-5135
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Searched: 2395520 seqs, 934235491 residues

Total number of hits satisfying chosen parameters: 3222406

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq.*
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8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	18.6	23.5	99	8	US-11-217-529-173876 Sequence 173876,
2	18.4	23.3	51	8	US-11-143-642-1090 Sequence 1090, Ap
3	18.2	23.0	50	6	US-10-554-711-648 Sequence 648, App
4	18.2	23.0	50	6	US-10-554-759-648 Sequence 648, App
5	17.8	22.5	77	7	US-11-357-615-25 Sequence 25, Appli
6	17.8	22.5	90	6	US-10-526-765-9 Sequence 9, Appli
7	17.2	21.8	25	9	US-11-348-413-618728 Sequence 618728,
8	17.2	21.8	66	9	US-11-375-551-85 Sequence 85, Appl
9	17.2	21.8	76	7	US-11-374-388-403 Sequence 403, App
10	17.2	21.8	99	6	US-10-531-545-10 Sequence 10, Appli
11	17	21.5	25	9	US-11-348-413-216548 Sequence 216548,
12	17	21.5	47	7	US-11-370-584-3264 Sequence 3264, Ap
13	17	21.5	93	8	US-11-243-296A-5 Sequence 5, Appli
14	16.6	21.0	25	9	US-11-348-413-216546 Sequence 216546,
15	16.6	21.0	25	9	US-11-348-413-216547 Sequence 216547,
16	16.6	21.0	80	9	US-11-267-769-77 Sequence 77, Appl
17	16.6	21.0	80	9	US-11-267-807-77 Sequence 77, Appl
18	16.6	21.0	90	7	US-11-280-456-20 Sequence 20, Appl
19	16.4	20.8	93	9	US-11-348-413-8848 Sequence 8848, Ap
20	16.4	20.8	93	9	US-11-348-413-9715 Sequence 9715, Ap
21	16.2	20.5	25	8	US-11-217-529-34950 Sequence 34950, A
22	16.2	20.5	25	9	US-11-348-413-425880 Sequence 425880,
23	16.2	20.5	25	9	US-11-348-413-425881 Sequence 425881,

24 16.2 20.5 25 9 US-11-348-413-425882 Sequence 425882,
25 16.2 20.5 25 9 US-11-348-413-425883 Sequence 425883,
26 16.2 20.5 25 9 US-11-348-413-425884 Sequence 425884,
27 16.2 20.5 25 9 US-11-348-413-1066900 Sequence 1066900,
28 16 20.3 25 9 US-11-348-413-216549 Sequence 216549,
29 16 20.3 25 9 US-11-348-413-998589 Sequence 998589,
30 16 20.3 62 7 US-11-292-078-13457 Sequence 13457, A
31 16 20.3 96 7 US-11-434-137-5433 Sequence 5433, Ap
32 16 20.3 96 7 US-11-434-184-5433 Sequence 5433, Ap
33 16 20.3 96 7 US-11-434-199-5433 Sequence 5433, Ap
34 16 20.3 96 7 US-11-434-203-5433 Sequence 5433, Ap
35 15.8 20.0 87 8 US-11-213-668-49 Sequence 49, Appl
36 15.8 20.0 93 8 US-11-213-668-32 Sequence 32, Appl
37 15.8 20.0 99 7 US-11-043-824-194 Sequence 194, App
38 15.6 19.7 25 9 US-11-348-413-511518 Sequence 511518,
39 15.6 19.7 25 9 US-11-348-413-546599 Sequence 546599,
40 15.6 19.7 25 9 US-11-348-413-638059 Sequence 638059,
41 15.6 19.7 25 9 US-11-348-413-1162729 Sequence 1162729,
42 15.6 19.7 25 9 US-11-348-413-1162730 Sequence 1162730,
43 15.6 19.7 25 9 US-11-348-413-1162731 Sequence 1162731,
44 15.6 19.7 25 9 US-11-348-413-1207851 Sequence 1207851,
45 15.6 19.7 25 9 US-11-348-413-1207852 Sequence 1207852,

ALIGNMENTS

RESULT 1
US-11-217-529-173876
; Sequence 173876, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 173876
; LENGTH: 99
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-173876
Query Match 23.5%; Score 18.6; DB 8; Length 99;
Best Local Similarity 39.4%; Pred. No. 2e+03; 9; Indels 0; Gaps 0;
Matches 13; Conservative 11; Mismatches 9;
QY 39 UVUACUUGGGGCGUAUUGUCUCUUCUUCG 71
::: |||||::: |||||::: |||||::: |||||
Db 39 TTGTTGGTGGGCTGCTTGGACCCATTTCG 71
RESULT 2
US-11-143-642-1090
; Sequence 1090, Application US/11143642
; Publication No. US20060099610A1
; GENERAL INFORMATION:
; APPLICANT: Jukka T. SALONEN et al.
; TITLE OF INVENTION: METHOD AND KIT FOR DETECTING A RISK OF ACUTE MYOCARDIAL INFARCTION
; FILE REFERENCE: 0933-0245FUS1
; CURRENT APPLICATION NUMBER: US/11/143,642
; CURRENT FILING DATE: 2005-06-03
; NUMBER OF SEQ ID NOS: 2039
; SOFTWARE: PatentIn version 3.3

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; SEQ ID NO 1090
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-143-642-1090

Query Match      23.3%; Score 18.4; DB 8; Length 51;
Best Local Similarity 41.3%; Pred. No. 2e+03;
Matches 19; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 32 CCCUUAUGAUCUCCGGCUCGUAUUGUCUCUCCUUUGGCCACCU 77
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Db 1 CCCTTAATAATATCTCGGCAGGTAYCGTAATCTCTTGGTCCCCCT 46

RESULT 3
US-10-554-711-648
; Sequence 648, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; FILE REFERENCE: as Molecular Markers of Cancer
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 648
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
US-10-554-711-648

Query Match      23.0%; Score 18.2; DB 6; Length 50;
Best Local Similarity 48.4%; Pred. No. 2.4e+03;
Matches 15; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 45 UUCGGCUCGUUAUUGUCUCUCUCCUUGGCCAC 75
::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db 12 TTGGGACTCGGACTGGCTCTCTTCCTGCGCCACC 42

RESULT 4
US-10-554-759-648
; Sequence 648, Application US/10554759
; Publication No. US20060177825A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; FILE REFERENCE: 21099.0077P1
; CURRENT APPLICATION NUMBER: US/10/554,759
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,801
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 648
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
OTHER INFORMATION: Synthetic Construct
US-10-554-759-648

Query Match      23.0%; Score 18.2; DB 6; Length 50;
Best Local Similarity 48.4%; Pred. No. 2.4e+03;
Matches 15; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 45 UUCGGCUCGUUAUUGUCUCUCUCCUUGGCCAC 75
::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db 12 TTGGGACTCGGACTGGCTCTCTTCCTGCGCCACC 42

RESULT 5
US-10-554-759-648
; Query Match      23.0%; Score 18.2; DB 6; Length 50;
; Best Local Similarity 48.4%; Pred. No. 2.4e+03;
; Matches 15; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 45 UUCGGCUCGUUAUUGUCUCUCUCCUUGGCCAC 75
::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db 12 TTGGGACTCGGACTGGCTCTCTTCCTGCGCCACC 42

RESULT 5
US-11-357-615-25
; Sequence 25, Application US/11357615
; Publication No. US20060188972A1
; GENERAL INFORMATION:
; APPLICANT: WOLFE, Alan P.
; APPLICANT: COLLINGWOOD, Trevor
; TITLE OF INVENTION: TARGETED MODIFICATION OF CHROMATIN STRUCTURE
; FILE REFERENCE: 8325-0014 / S14-US1
; CURRENT APPLICATION NUMBER: US/11/357,615
; CURRENT FILING DATE: 2006-02-16
; PRIOR APPLICATION NUMBER: US/09/844,508
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/200,590
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/228,523
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 77
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fragment
; OTHER INFORMATION: encoding DGGGS linker, 3' to 5'
US-11-357-615-25

Query Match      22.5%; Score 17.8; DB 7; Length 77;
Best Local Similarity 37.8%; Pred. No. 3.8e+03;
Matches 14; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 40 UGUACUUGCGCUCGUUAUUGUCUCUCUCCUUGGCCACC 76
::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db 3 TGTAGTTTGCGTCTCTTCTTCTCTGCGGCCACC 39

RESULT 6
US-10-526-765-9/c
; Sequence 9, Application US/10526765
; Publication No. US20060121049A1
; GENERAL INFORMATION:
; APPLICANT: LETOURNEUR, Odile
; TITLE OF INVENTION: CHIMERIC RECOMBINANT PROTEIN AND IN VITRO DIAGNOSIS
; FILE REFERENCE: 122802
; CURRENT APPLICATION NUMBER: US/10/526,765
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: PCT/FR03/02712
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: FR 02/11485
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 90
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-10-526-765-9
```

```

Qy 35 UUAUUGUACUUGGGGCUUAUUGUCUUCUUCUUGGCGACCUCC 79
Db 45 TTTATATAAATTCACCTTCTCCAATTGTCCCTCATATCTCTCTCTCC 1

RESULT 7
US-11-348-413-618728/c
; Sequence 618728, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 618728
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 370; WAN01UJA4-5_at; Start 75; Stop 99;
; OTHER INFORMATION: 011101100000000
US-11-348-413-618728

Query Match 21.8%; Score 17.2; DB 9; Length 25;
Best Local Similarity 40.9%; Pred. No. 4.5e+03;
Matches 9; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 50 GCUCGUATUUGUCUUCUUCUG 71
Db 25 GTCGTATTTCCTCATTTCC 4

RESULT 8
US-11-375-551-85
; Sequence 85, Application US/11375551
; Publication No. US20060158434A1
; GENERAL INFORMATION:
; APPLICANT: Bintrim, Scott
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Apel-Birkhold, Patricia
; APPLICANT: Schafer, Barry
; APPLICANT: Bevan, Scott
; APPLICANT: Young, Scott
; APPLICANT: Guo, Lining
; TITLE OF INVENTION: Xenorhabdus TC Proteins and Genes for Pest Control
; FILE REFERENCE: DAS-105X
; CURRENT APPLICATION NUMBER: US/11/375,551
; CURRENT FILING DATE: 2006-03-14
; PRIOR APPLICATION NUMBER: US/10/753,901
; PRIOR FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/441,717
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 85
; LENGTH: 66

```

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Reverse primer sequence used to amplify XptB1
US-11-375-551-85

Query Match      21.8%; Score 17.2; DB 9; Length 66;
Best Local Similarity 36.8%; Pred. No. 6e+03;
Matches 14; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY    24 GCUCUGGCCCCUUAUAGUACUUGCGGCGCUGAUUUGUC 61
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB    1  GCTGCAGACAGTAATATTATGCTTCGGATTCAATTATGAC 38

RESULT 9
US-11-374-388-403
; Sequence 403, Application US/11374388
; Publication No. US20060193870A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secret, Heather
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.547C6
; CURRENT APPLICATION NUMBER: US/11/374,388
; CURRENT FILING DATE: 2006-03-13
; PRIOR APPLICATION NUMBER: US 10/099,926
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: US 10/033,528
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: US 09/920,300
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/302,051
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/279,763
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/223,283
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 1982
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 403
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7, 11, 18, 30, 31, 46, 47, 61, 62
; OTHER INFORMATION: n = A,T,C or G
US-11-374-388-403

Query Match      21.8%; Score 17.2; DB 7; Length 76;
Best Local Similarity 51.4%; Pred. No. 6.3e+03;
Matches 18; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY    7 CGGGGGAGACGACGAGCGGCUUCGCCCCCUAAUUG 41
      ||||| :||||| :||| :||| :||| :||| :||| :||| :||| :|||
DB    1  CTGGGANATGCGAGCTNCTCTGGCATCTNNATGG 35

RESULT 10
US-10-531-545-10
; Sequence 10, Application US/10531545
; Publication No. US20060183106A1
; GENERAL INFORMATION:
; APPLICANT: SIDDQUI-JAIN, Adam
; TITLE OF INVENTION: PROCESSES FOR IDENTIFYING
; FILE REFERENCE: QUADRUPEX-TARGETED ANTIVIRAL MOLECULES
; CURRENT APPLICATION NUMBER: US/10/531,545

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Reverse primer sequence used to amplify XptB1
US-11-375-551-85

Query Match      21.8%; Score 17.2; DB 9; Length 66;
Best Local Similarity 36.8%; Pred. No. 6e+03;
Matches 14; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY    24 GCUCUGGCCCCUUAUAGUACUUGCGGCGCUGAUUUGUC 61
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB    1 GCTGCAGACAGTAATATTATGCTTCGGATTCAATTATGAC 38

RESULT 9
US-11-374-388-403
; Sequence 403, Application US/11374388
; Publication No. US20060193870A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secret, Heather
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.547C6
; CURRENT APPLICATION NUMBER: US/11/374,388
; CURRENT FILING DATE: 2006-03-13
; PRIOR APPLICATION NUMBER: US 10/099,926
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: US 10/033,528
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: US 09/920,300
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/302,051
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/279,763
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/223,283
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 1982
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 403
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7, 11, 18, 30, 31, 46, 47, 61, 62
; OTHER INFORMATION: n = A,T,C or G
US-11-374-388-403

Query Match      21.8%; Score 17.2; DB 7; Length 76;
Best Local Similarity 51.4%; Pred. No. 6.3e+03;
Matches 18; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY    7 CGGGGGAGACGACGAGCGGCUUCGCCCCCUAAUUG 41
      ||||| :||||| :||| :||| :||| :||| :||| :||| :||| :|||
DB    1 CTGGGANATGCGAGCTNCTCTGGCATCTNNATGG 35

RESULT 10
US-10-531-545-10
; Sequence 10, Application US/10531545
; Publication No. US20060183106A1
; GENERAL INFORMATION:
; APPLICANT: SIDDQUI-JAIN, Adam
; TITLE OF INVENTION: PROCESSES FOR IDENTIFYING
; FILE REFERENCE: 53223200900
; CURRENT APPLICATION NUMBER: US/10/531,545

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; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: PCT/US03/33366
; PRIOR FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US 60/419,456
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 99
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-531-545-10

Query Match      21.8%; Score 17.2; DB 6; Length 99;
Best Local Similarity 40.3%; Pred. No. 6.8e+03;
Matches 25; Conservative 9; Mismatches 28; Indels 0; Gaps 0;

QY 1 GGAGGGGGGGGAGACGAGCGGCGUCUGCCCUAAUUGUACUUGCGGCGUGUAUUGU 60
Db 19 GGAGGGTGGGGAGGTGGGGAAGTTAGGACACGCAATGCTATAGTGATGATTAG 78

QY 61 CU 62
   | :
Db 79 CT 80

RESULT 11
US-11-348-413-216548/c
; Sequence 216548, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; PRIOR FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 216548
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 6358; WANO1UKNQ; Start 1515; Stop 1539;
; OTHER INFORMATION: 000000011100000
US-11-348-413-216548

Query Match      21.5%; Score 17; DB 9; Length 25;
Best Local Similarity 36.0%; Pred. No. 5.3e+03;
Matches 9; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 36 UAAUUGUACUUGCGGCGUGUAUUGU 60
Db 25 TGATTGTAATCTGGATGGTATTGT 1

RESULT 12
US-11-370-584-3264/c
; Sequence 3264, Application US/11370584
```

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; Publication No. US20060177863A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/11/370,584
; CURRENT FILING DATE: 2006-03-08
; PRIOR APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3264
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-2832-152 : polymorphic base C or T
US-11-370-584-3264

Query Match      21.5%; Score 17; DB 7; Length 47;
Best Local Similarity 89.5%; Pred. No. 6.4e+03;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGGGCGGGGAGAGACG 19
Db 38 GGAGGGCGAGGAGRGACG 20

RESULT 13
US-11-243-296A-5
; Sequence 5, Application US/11243296A
; Publication No. US20060112449A1
; GENERAL INFORMATION:
; APPLICANT: Van der Linden, C.G.
; APPLICANT: Alwee, Sharifah S.R.S.
; APPLICANT: Smuiders, J.M.
; APPLICANT: Choo, Cheah S.
; TITLE OF INVENTION: Novel B-type gene from oil palm
; FILE REFERENCE: SHDEL2.002AUS
; CURRENT APPLICATION NUMBER: US/11/243,296A
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: MY PI 20044004
; PRIOR FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 93
; TYPE: DNA
; ORGANISM: Elaeis guineensis
US-11-243-296A-5

Query Match      21.5%; Score 17; DB 8; Length 93;
Best Local Similarity 31.7%; Pred. No. 7.9e+03;
Matches 13; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 25 CUCUGGCCCUAAUUGUACUUGCGGCGUGUAUUGUCUC 65
Db 7 CTCGCCCCCTCTATCTCTCTCGGTGCTCTTCTTCTC 47

RESULT 14
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US-11-348-413-216546/c
; Sequence 216546, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 216546
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)-(25)
; OTHER INFORMATION: SEQ ID NO: 6358; WAN01UKNQ; Start 1513; Stop 1537;
; OTHER INFORMATION: 000000011100000
US-11-348-413-216546

Query Match 21.0%; Score 16.6; DB 9; Length 25;
Best Local Similarity 39.1%; Pred.No.7.5e+03;
Matches 9; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 38 AUUGUACUUGCGGCGUUAUGU 60
|::||::||::||::||::||::||
Db 25 ATTGTAATTCGGATGGTATTGT 3

RESULT 15
US-11-348-413-216547/c
; Sequence 216547, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 216547
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)-(25)
; OTHER INFORMATION: SEQ ID NO: 6358; WAN01UKNQ; Start 1514; Stop 1538;
; OTHER INFORMATION: 000000011100000
US-11-348-413-216547

Query Match 21.0%; Score 16.6; DB 9; Length 25;
Best Local Similarity 39.1%; Pred.No.7.5e+03;
Matches 9; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 38 AUUGUACUUGCGGCGUUAUGU 60
|::||::||::||::||::||::||
Db 24 ATTGTAATTCGGATGGTATTGT 2

Search completed: October 16, 2006, 14:51:29
Job time : 140 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 13:53:09 ; Search time 125.594 Seconds
(without alignments)
1332.341 Million cell updates/sec

Title: US-10-604-726A-5136

Perfect score: 24

Sequence: 1 uauugucucuccuuuugccaccuc 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 4443654

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_8.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*
- 15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15.8	65.8	24	4	AAD21686
C 2	15.6	65.0	24	2	AAQ44801
C 3	15.6	65.0	24	2	AAQ44806
C 4	15.6	65.0	24	2	AAT92274
C 5	15.6	65.0	24	2	AAV31726
C 6	15.6	65.0	24	2	AAV31731
C 7	15.6	65.0	24	2	AAQ4070
C 8	15.6	65.0	24	2	AAQ4075
C 9	15.6	65.0	25	15	AE94315
C 10	15.2	63.3	21	7	ADI94591
C 11	15.2	63.3	22	7	ADI94589
C 12	15.2	63.3	27	7	ADI94590
C 13	15.2	63.3	28	7	ADI94588
C 14	14.8	61.7	29	2	AAV91451
C 15	14.8	61.7	29	3	AAF01081
C 16	14.6	60.8	30	14	ADX99968
C 17	14.4	60.0	18	2	AAQ5826
C 18	14.4	60.0	20	7	ADI94593

C 19	14.4	60.0	23	2	AAQ85989
C 20	14.4	60.0	26	7	ADI94592
C 21	14.2	59.2	21	2	AAQ56946
C 22	14.2	59.2	21	15	AEF13105
C 23	14.2	59.2	25	10	ADC05103
C 24	14.2	59.2	25	10	ADC05104
C 25	14.2	59.2	25	10	ADC05109
C 26	14.2	59.2	25	10	ADC05105
C 27	14.2	59.2	25	10	ADC05108
C 28	14.2	59.2	25	10	ADC05106
C 29	14.2	59.2	25	10	ADC05107
C 30	14	58.3	24	2	AAQ38850
C 31	14	58.3	24	2	AAQ44802
C 32	14	58.3	24	2	AAQ99270
C 33	14	58.3	24	2	AAV31727
C 34	14	58.3	24	2	AAQ04071
C 35	14	58.3	24	5	AAH48099
C 36	14	58.3	24	14	AEC26021
C 37	14	58.3	24	14	AEC28387
C 38	14	58.3	25	9	ACK16088
C 39	14	58.3	30	8	ACD27983
C 40	14	58.3	30	10	ADA09553
C 41	13.8	57.5	17	10	ADC03597
C 42	13.8	57.5	20	2	AAQ94034
C 43	13.8	57.5	20	8	ABX04519
C 44	13.8	57.5	20	10	ADC01938
C 45	13.8	57.5	20	10	AAQ59884

ALIGNMENTS

RESULT 1
AAD21686/c
ID AAD21686 standard; DNA; 24 BP.
XX AAD21686;
AC AAD21686;
DT 28-JAN-2002 (first entry)
XX Imperfect direct repeat #1 of human RPGR exon ORF15 repetitive sequence.

DE Human; mutation; retinitis pigmentosa GTPase regulator; RPGR; genotyping;
KW open reading frame; ORF; X-linked retinitis pigmentosa; XLRP;
KW gene therapy; screening; forensic analysis; ds.
XX Homo sapiens.
XX WO200177380-A2.
PD 18-OCT-2001.
XX 10-APR-2001; 2001WO-GB001622.
XX 10-APR-2000; 2000GB-00008801.
XX (MEDI-) MEDICAL RES COUNCIL.
XX Wright A;
XX WPI; 2001-663057/76.

Diagnosing disease or predisposition to disease, associated with disease causing mutations in retinitis pigmentosa GTPase regulator gene by genotyping ORF15 of the gene, and determining presence of mutations.

Disclosure; Fig 4E; 100pp; English.

The present invention relates to a method for diagnosing disease or predisposition to a disease, associated with a disease causing mutations in a retinitis pigmentosa GTPase regulator (RPGR) gene involves genotyping a RPGR gene, and determining whether the genotype comprises a disease causing mutations, where the risk genotype is present within open

CC reading frame (ORF)15 of the RPGR gene. The method is useful for
 CC detecting a certain disease state e.g., X-linked retinitis pigmentosa
 CC (XLRP). The kit is useful for detecting and measuring disease causing
 CC mutations in biological fluids and tissues and for localising mutation in
 CC tissues. The mutant RPGR gene is useful in gene therapy techniques and
 CC for screening agents capable of affecting the expression of the sequences
 CC and/or the biological activity of mutant RPGR. They are preferably useful
 CC for identifying agonists and antagonists of RPGR. The mutant RPGR gene is
 CC also useful in identification of potential pharmaceutical targets in high
 CC throughput screening assays and forensic analysis. The present sequence
 CC is the imperfect direct repeat of human RPGR exon ORF15 repetitive DNA
 XX
 SQ Sequence 24 BP; 10 A; 0 C; 14 G; 0 T; 0 U; 0 Other;

Query Match 65.8%; Score 15.8; DB 4; Length 24;
 Best Local Similarity 52.6%; Pred. No. 3.7e+03;
 Matches 10; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 6 UCUCUCUUCGCCACCUC 24
 Db 19 TCTCTCTCTCCCTCCTC 1

RESULT 2
 AAQ44801/c
 ID AAQ44801 standard; DNA; 24 BP.

XX AC AAQ44801;

XX 25-MAR-2003 (revised)
 DT 28-SEP-1994 (first entry)

XX Purine-rich PUR element.

XX Single-strand binding protein; PUR protein; cellular oncogene;
 KW eukaryotic origin of replication; gene amplification; cancer cell;
 KW retinoblastoma protein; helix-destabilising protein; inhibitor;
 KW hyperproliferation; ss.

XX Homo sapiens.

XX WO9405689-A1.

PD 17-MAR-1994.

XX 27-AUG-1993; 93WO-US008102.

XX 28-AUG-1992; 92US-00938189.

PR 02-FEB-1993; 93US-00014943.

XX (MOUN) MOUNT SINAI SCHOOL MEDICINE.

XX Johnson EM, Bergemann AD;

XX WPI; 1994-101114/12.

XX Cloning and expression of PUR protein, involved in regulation of DNA
 PT replication - also oligo:nucleotide(s) and antibodies for use in the
 PT treatment of proliferative diseases, e.g. cancer.

XX Claim 6; Page 65; 97pp; English.

XX PUR elements are purine-rich 24 nucleotide DNA sequences which occur at
 CC eukaryotic origins of replication and 5' flanking regions of some
 CC cellular oncogenes. The PUR protein (AAR50310) was originally identified
 CC as a 27kD HeLa cell nuclear factor that bound in a sequence-specific
 CC manner to a major site of DNA bending located 1.6kb upstream of the
 CC transcription start site of the human c-myc gene; the site recognised by
 CC PUR protein had the sequence AAQ44801. (Updated on 25-MAR-2003 to correct
 CC PN field.)

XX Sequence 24 BP; 8 A; 0 C; 14 G; 2 T; 0 U; 0 Other;

Query Match 65.0%; Score 15.6; DB 2; Length 24;
 Best Local Similarity 50.0%; Pred. No. 4.5e+03;
 Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 UUGUCUCUUCGCCACCUC 24
 Db 23 TTTTCTCTCTCCCTCACCACCTC 2

RESULT 3
 AAQ44806
 ID AAQ44806 standard; DNA; 24 BP.

XX AC AAQ44806;

XX 25-MAR-2003 (revised)

DT 28-SEP-1994 (first entry)

XX Oligonucleotide MR0700 used in characterising c-myc PUR element.

XX Single-strand binding protein; PUR protein; cellular oncogene;
 KW eukaryotic origin of replication; gene amplification; cancer cell;
 KW retinoblastoma protein; helix-destabilising protein; inhibitor;
 KW hyperproliferation; c-myc; ss.

XX Synthetic.

XX WO9405689-A1.

XX 17-MAR-1994.

XX 27-AUG-1993; 93WO-US008102.

XX 28-AUG-1992; 92US-00938189.

PR 02-FEB-1993; 93US-00014943.

XX (MOUN) MOUNT SINAI SCHOOL MEDICINE.

XX Johnson EM, Bergemann AD;

XX WPI; 1994-101114/12.

XX Cloning and expression of PUR protein, involved in regulation of DNA
 PT replication - also oligo:nucleotide(s) and antibodies for use in the
 PT treatment of proliferative diseases, e.g. cancer.

XX Example 1; Page 37; 97pp; English.

XX Oligonucleotides AAQ44802-Q44809 were used in the characterisation of a
 CC sequence element found 1.6kb upstream of the cellular c-myc gene. The PUR
 CC element (see AAQ44801) is located in a region of DNA bending activity
 CC which is a structural feature often associated with origins of DNA
 CC replication. The PUR protein AAR50310 binds to the PUR element. (Updated
 CC on 25-MAR-2003 to correct PN field.)

XX Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 65.0%; Score 15.6; DB 2; Length 24;
 Best Local Similarity 50.0%; Pred. No. 4.5e+03;
 Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 UUGUCUCUUCGCCACCUC 24
 Db 2 TTTTCTCTCTCCCTCACCACCTC 23

RESULT 4
 AAT99274
 ID AAT99274 standard; DNA; 24 BP.

XX AC AAT99274;

XX 15-APR-1998 (first entry)

XX DE Human PUR-alpha gene probe MR0700.
 XX PI
 KW PUR element; human; c-myc; inhibitor; hyperproliferative disease; ss;
 KW cancer; probe; hybridisation.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5672479-A.
 XX
 PD 30-SEP-1997.
 XX
 PF 07-JUN-1995; 95US-00486421.
 XX
 PR 28-AUG-1992; 92US-00938189.
 PR 02-FEB-1993; 93US-00014943.
 PR 06-JUN-1995; 95US-00470911.
 XX
 PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
 XX
 PI Bergemann AD, Johnson EM;
 XX
 DR WPI; 1997-488859/45.
 XX
 XX Assays for PUR protein ligands or modulators - using immobilised PUR
 PT protein or fragments, to treat hyper-proliferative diseases, e.g. cancer.
 XX
 PS Example; Col 26; 64pp; English.
 XX
 CC The probes AAT99270-799277 were used to screen for positive clones
 CC containing a 467 bp Sau3AI fragment of the human c-myc upstream region
 CC cloned into pUC19. Isolated sequences were then used as probes to screen
 CC an expression library for sequences encoding the PUR protein. The PUR
 CC sequence can be used to identify chemical or biological compounds that
 CC bind to PUR or binding fragments of PUR. Inhibitors of PUR activity may
 CC be used to treat hyperproliferative diseases such as cancer
 XX
 SQ Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;
 XX
 Query Match 65.0%; Score 15.6; DB 2; Length 24;
 Best Local Similarity 50.0%; Pred. No. 4.5e+03;
 Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
 QY 3 UUGUCUCUCUUCGCCACCUC 24
 Db :::::|||||
 2 TTTTCTCTCCCTCCACCCTC 23
 RESULT 5
 AAV31726/c
 ID AAV31726 standard; DNA; 24 BP.
 XX
 AC AAV31726;
 XX
 DT 24-SEP-1998 (first entry)
 XX
 DE Nucleotide sequence of the PUR element.
 XX
 KW PUR-alpha gene; inhibition; viral infection; cancer; PUR element;
 KW hyperproliferative disease; ss.
 XX
 OS Homo sapiens.
 OS
 PN US5756684-A.
 XX
 PD 26-MAY-1998.
 XX
 PF 06-JUN-1995; 95US-00470911.
 XX
 PR 28-AUG-1992; 92US-00938189.
 PR 02-FEB-1993; 93US-00014943.
 XX
 PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
 XX
 PI Bergemann AD, Johnson EM;
 XX
 DR WPI; 1998-321632/28.
 XX
 PT PUR protein and its fragments - that inhibit PUR protein binding to PUR
 KW element or other proteins.
 XX
 PS Example 6.1.1; Col 27; 63pp; English.
 XX
 CC This is the nucleotide sequence of an oligonucleotide used in the method
 CC of the invention, involving the use of the PUR protein and its fragments,
 CC which inhibit PUR protein binding to PUR element or other proteins.
 CC Inhibitors of PUR activity may be useful for treating viral infections
 CC and hyperproliferative diseases such as cancer
 XX
 SQ Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;
 XX
 Query Match 65.0%; Score 15.6; DB 2; Length 24;
 Best Local Similarity 50.0%; Pred. No. 4.5e+03;
 Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
 QY 3 UUGUCUCUCUUCGCCACCUC 24
 Db :::::|||||
 2 TTTTCTCTCCCTCCACCCTC 23

PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
 XX
 PI Bergemann AD, Johnson EM;
 XX
 DR WPI; 1998-321632/28.
 XX
 PT PUR protein and its fragments - that inhibit PUR protein binding to PUR
 PT element or other proteins.
 XX
 PS Disclosure; Col 12; 63pp; English.
 XX
 CC This is the nucleotide sequence of the PUR element used in the method of
 CC the invention, involving the use of the PUR protein and its fragments,
 CC which inhibit PUR protein binding to PUR element or other proteins.
 CC Inhibitors of PUR activity may be useful for treating viral infections
 CC and hyperproliferative diseases such as cancer
 XX
 SQ Sequence 24 BP; 8 A; 0 C; 14 G; 2 T; 0 U; 0 Other;
 XX
 Query Match 65.0%; Score 15.6; DB 2; Length 24;
 Best Local Similarity 50.0%; Pred. No. 4.5e+03;
 Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
 QY 3 UUGUCUCUCUUCGCCACCUC 24
 Db :::::|||||
 23 TTTTCTCTCCCTCCACCCTC 2
 RESULT 6
 AAV31731
 ID AAV31731 standard; DNA; 24 BP.
 XX
 AC AAV31731;
 XX
 DT 24-SEP-1998 (first entry)
 XX
 DE Nucleotide sequence of the oligonucleotide MR0700.
 XX
 KW PUR-alpha gene; inhibition; viral infection; cancer; PUR element;
 KW hyperproliferative disease; ss.
 XX
 OS Synthetic.
 OS
 PN US5756684-A.
 XX
 PD 26-MAY-1998.
 XX
 PF 06-JUN-1995; 95US-00470911.
 XX
 PR 28-AUG-1992; 92US-00938189.
 PR 02-FEB-1993; 93US-00014943.
 XX
 PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
 XX
 PI Bergemann AD, Johnson EM;
 XX
 DR WPI; 1998-321632/28.
 XX
 PT PUR protein and its fragments - that inhibit PUR protein binding to PUR
 PT element or other proteins.
 XX
 PS Example 6.1.1; Col 27; 63pp; English.
 XX
 CC This is the nucleotide sequence of an oligonucleotide used in the method
 CC of the invention, involving the use of the PUR protein and its fragments,
 CC which inhibit PUR protein binding to PUR element or other proteins.
 CC Inhibitors of PUR activity may be useful for treating viral infections
 CC and hyperproliferative diseases such as cancer
 XX
 SQ Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;
 XX
 Query Match 65.0%; Score 15.6; DB 2; Length 24;
 Best Local Similarity 50.0%; Pred. No. 4.5e+03;

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Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 3 UUGUCUCUCCUUGGCCACCUC 24
Db 2 TTTTCTCTCCCTCCACCACCTC 23

RESULT 7
AAX04070/c
ID AAX04070 standard; DNA; 24 BP.
XX AC
XX AAX04070;
XX 12-APR-1999 (first entry)
XX DE
XX Oligonucleotide MF0677 used in PUR identification/characterisation.
XX KW
XX PUR element; PUR-alpha; hyperproliferative disease; cancer; human;
XX monoclonal antibody; identification; characterisation; ss.
XX OS
XX Synthetic.
XX OS
XX Homo sapiens.
XX PN
XX US5869622-A.
XX PD
XX 09-FEB-1999.
XX PF
XX 07-JUN-1995; 95US-00486809.
XX PR
XX 28-AUG-1992; 92US-00938189.
XX PR
XX 02-FEB-1993; 93US-00014943.
XX PR
XX 06-JUN-1995; 95US-00470911.
XX PA
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX PI
XX Bergemann AD, Johnson EM;
XX WPI; 1999-152881/13.
XX DR
XX Monoclonal antibody specific for PUR protein - useful for treating
XX cancer.
XX PT
XX Example; Col 27; 64pp; English.
XX PS
XX The present invention describes a monoclonal antibody that specifically
XX binds to an epitope of the PUR protein. Antibodies that bind to the PUR
XX protein and neutralise PUR activity may be used to treat
XX hyperproliferative diseases such as cancer. PUR antibodies may be used
XX diagnostically to detect aberrant expression of the PUR protein and/or
XX mutations in the PUR gene. The present sequence represents an
XX oligonucleotide used in the identification and characterisation of the
XX PUR protein and its sequence element PUR repeat, in an example from the
XX present invention
XX SQ
XX Sequence 24 BP; 8 A; 0 C; 14 G; 2 T; 0 U; 0 Other;

Query Match 65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 3 UUGUCUCUCCUUGGCCACCUC 24
Db 2 TTTTCTCTCCCTCCACCACCTC 23

RESULT 8
AAX04075
ID AAX04075 standard; DNA; 24 BP.
XX AC
XX AAX04075;
XX 12-APR-1999 (first entry)
XX DE
XX Chromatin; DNA hybridization; DNA amplification; DNA microarray;
XX diagnosis; ss; primer; PCR; OLIG2.
XX OS
XX Homo sapiens.
XX PN
XX WO2005118873-A2.
XX PD
XX 15-DEC-2005.
XX PF
XX 31-MAY-2005; 2005WO-US019150.
XX PR
XX 28-MAY-2004; 2004US-0575478P.
XX

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DE Oligonucleotide MR0700 used in PUR identification/characterisation.
XX PUR element; PUR-alpha; hyperproliferative disease; cancer; human;
XX monoclonal antibody; identification; characterisation; ss.
XX OS
XX Synthetic.
XX OS
XX Homo sapiens.
XX PN
XX US5869622-A.
XX PD
XX 09-FEB-1999.
XX PF
XX 07-JUN-1995; 95US-00486809.
XX PR
XX 28-AUG-1992; 92US-00938189.
XX PR
XX 02-FEB-1993; 93US-00014943.
XX PR
XX 06-JUN-1995; 95US-00470911.
XX PA
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX PI
XX Bergemann AD, Johnson EM;
XX WPI; 1999-152881/13.
XX DR
XX Monoclonal antibody specific for PUR protein - useful for treating
XX cancer.
XX PT
XX Example; Col 27; 64pp; English.
XX PS
XX The present invention describes a monoclonal antibody that specifically
XX binds to an epitope of the PUR protein. Antibodies that bind to the PUR
XX protein and neutralise PUR activity may be used to treat
XX hyperproliferative diseases such as cancer. PUR antibodies may be used
XX diagnostically to detect aberrant expression of the PUR protein and/or
XX mutations in the PUR gene. The present sequence represents an
XX oligonucleotide used in the identification and characterisation of the
XX PUR protein and its sequence element PUR repeat, in an example from the
XX present invention
XX SQ
XX Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 3 UUGUCUCUCCUUGGCCACCUC 24
Db 2 TTTTCTCTCCCTCCACCACCTC 23

RESULT 9
AEE94315/c
ID AEE94315 standard; DNA; 25 BP.
XX AC
XX AEE94315;
XX 23-FEB-2006 (first entry)
XX DT
XX 3' primer for PCR of DNase I treated OLIG2 chromatin.
XX DE
XX Chromatin; DNA hybridization; DNA amplification; DNA microarray;
XX diagnosis; ss; primer; PCR; OLIG2.
XX OS
XX Homo sapiens.
XX PN
XX WO2005118873-A2.
XX PD
XX 15-DEC-2005.
XX PF
XX 31-MAY-2005; 2005WO-US019150.
XX PR
XX 28-MAY-2004; 2004US-0575478P.
XX

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PA	(CEMT-) CEMINES INC.	XX	24-MAY-2000; 2000US-00577304.
PI	Neuman T;	PR	11-JAN-2001; 2001US-00758282.
XX		PR	24-MAY-2001; 2001US-00864426.
DR	WPI; 2006-047578/05.	PR	24-MAY-2001; 2001US-00864636.
XX		XX	(THIR-) THIRD WAVE TECHNOLOGIES INC.
PT	Detecting open chromatin comprises determining hybridization of the	PA	Allawi H, Bartholomay CT, Chehak L, Curtis ML, Eis PS, Hall JG;
PT	capture probe to the treated- and untreated-sample amplification	XX	Ip HS, Kaiser M, Kwiatkowski RW, Lukowiak AA, Lyamichiev V, Ma W;
XX	products.	PI	Olson-Munoz MC, Olson SM, Schaefer JJ, Skrzypczynski Z, Takova TV;
PS	Example 1; Page 37; 43pp; English.	PI	Vedvik KL, Lyamichiev NE, Neri BP;
XX		XX	WPI; 2002-083110/11.
CC	The new invention relates to detecting open chromatin in genomic DNA by	DR	Composition comprising enzyme which comprises heterologous functional
CC	determining the hybridization of a capture probe to a treated sample	XX	domain that provides altered functionality in nucleic acid cleavage
CC	amplification products and the untreated sample amplification products.	PT	assay, useful for cleaving nucleic acid, and detecting presence of RNA
CC	Specifically, the method comprises preparing a chromatin sample from	PT	target.
CC	cells, the chromatin sample comprising genomic DNA segments or genomic	XX	Claim 95; SEQ ID NO 2144; 1266pp; English.
CC	DNA with one or more open chromatin sites; treating a first portion of	XX	This invention describes a novel composition comprising an enzyme which
CC	the chromatin sample with an open chromatin DNA cleaving agent to produce	CC	contains a heterologous functional domain that provides altered
CC	fragments; performing a first amplification reaction using the fragments	CC	functionality in a nucleic acid cleavage assay. The enzyme comprises a 5'
CC	as a substrate, to produce treated-sample amplification products;	CC	nuclease, preferably a thermostable 5' nuclease, or a polymerase which is
CC	performing a second amplification reaction using a second portion of the	CC	altered in sequence related to a naturally occurring sequence of a
CC	chromatin sample, where the second portion is not treated with the open	CC	polymerase such that it inhibits reduced DNA synthetic activity from that
CC	chromatin DNA cleaving agent, to produce untreated-sample amplification	CC	of the naturally occurring polymerase. Preferably the polymerase is a
CC	products; incubating the treated-sample amplification products and the	CC	thermostable polymerase from a Thermus species such as T. aquaticus, T.
CC	untreated-sample amplification products with a capture probe; and	CC	flavus, T. thermophilus, T. filiformis or T. scotoductus. The enzyme
CC	determining the hybridization of the capture probe to the products, where	CC	comprises a heterologous functional domain, an amino acid sequence that
CC	the untreated-sample amplification products hybridize to the capture	CC	provides an improved substrate binding activity in the nucleic acid
CC	probe, and where reduced hybridization of the capture probe to the	CC	cleavage assay and an amino acid sequence that provides improved
CC	treated-sample amplification products as compared to the hybridization of	CC	background specificity in the nucleic acid cleavage assay. The invasive
CC	the capture probe to the untreated-sample amplification products	CC	cleavage structure comprises a RNA target nucleic acid (a cytochrome
CC	indicates the presence of open chromatin in the genomic DNA. Also given	CC	P450, or cytochrome RNA). Cleavage of the invasive cleavage structure
CC	is a chromatin state profiling array, for detecting the presence of open	CC	generates a non-target cleavage product, which is then detected by
CC	chromatin in genomic DNA. The methods and chromatin state profiling array	CC	detecting fluorescence, mass or fluorescence energy transfer or by
CC	are useful for detecting open chromatin in genomic DNA, used in	CC	detecting radioactivity luminescence, phosphorescence, fluorescence
CC	diagnostic and prognostic methods, and are useful for monitoring	CC	polarisation or charge. The enzyme is useful for cleaving a nucleic acid
CC	treatment and evaluating the response of cells and patients to candidate	CC	which involves exposing a sample (a cell lysate) comprising substrate
CC	or established therapeutic agents. The present sequence is a 3' reverse	CC	nucleic acid to the enzyme which produces at least one detectable
CC	primer for one-sided PCR amplification of DNase I treated chromatin	CC	cleavage product. The enzyme is employed for detecting target DNAs and
XX	fragments, deposited on a chromatin profiling array.	CC	RNAs comprising wild-type and mutant alleles of genes including genes
XX		CC	from humans, other animal or plants that are or may be associated with
XX		CC	disease or other conditions. In addition, the enzymes may be useful for
XX		CC	detecting and identifying strains of microorganisms including bacteria,
XX		CC	fungi, protozoa, ciliates and viruses, preferably detecting and
XX		CC	identifying viruses having RNA genomes, such as hepatitis C and human
XX		CC	immunodeficiency virus.
XX		XX	
SQ	Sequence 25 BP; 13 A; 0 C; 11 G; 1 T; 0 U; 0 Other;	SQ	Sequence 21 BP; 9 A; 3 C; 8 G; 1 T; 0 U; 0 Other;
	Query Match 65.0%; Score 15.6; DB 15; Length 25;		Query Match 63.3%; Score 15.2; DB 7; Length 21;
	Best Local Similarity 40.9%; Pred. No. 4.5e+03;		Best Local Similarity 50.0%; Pred. No. 6.6e+03;
	Matches 9; Conservative 9; Mismatches 4; Indels 0; Gaps 0;		Matches 10; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
QY	2 AUGUCUCUCCUUCGCCACCU 23	QY	5 GUCUCUCCUUCGCCACCU 24
DB	22 ATTCTCTCTTTTCTCTCT 1	DB	20 GTCTCTCTTTTCCAGTTC 1
	RESULT 10		RESULT 11
AD194591/c		AD194589/c	
ID	AD194591 standard; DNA; 21 BP.	ID	AD194589 standard; DNA; 22 BP.
XX		XX	
AC	AD194591;	AC	AD194589;
XX		XX	
DT	04-NOV-2004 (first entry)	DT	04-NOV-2004 (first entry)
XX		XX	
DE	Murine IFN-gamma associated probe SEQ ID 2144.	DE	Murine IFN-gamma associated probe SEQ ID 2142.
XX		XX	
KW	functional domain; nucleic acid cleavage assay; nuclease; polymerase;		
KW	detection; microorganism; RNA genome; hepatitis C;		
KW	human immunodeficiency virus; 88; probe.		
XX			
OS	Mus musculus.		
XX			
PN	WO200190337-A2.		
XX			
PD	29-NOV-2001.		
XX			
PF	24-MAY-2001; 2001WO-US017086.		

CC	polarisation or charge. The enzyme is useful for cleaving a nucleic acid
CC	which involves exposing a sample (a cell lysate) comprising substrate
CC	nucleic acid to the enzyme which produces at least one detectable
CC	cleavage product. The enzyme is employed for detecting target DNAs and
CC	RNAs comprising wild-type and mutant alleles of genes including genes
CC	from humans, other animal or plants that are or may be associated with
CC	disease or other conditions. In addition, the enzymes may be useful for
CC	detecting and identifying strains of microorganisms including bacteria,
CC	fungi, protozoa, ciliates and viruses, preferably detecting and
CC	identifying viruses having RNA genomes, such as hepatitis C and human
CC	immunodeficiency virus.
XX	
SQ	Sequence 28 BP; 3 A; 11 C; 4 G; 10 T; 0 U; 0 Other;
	Query Match 63.3%; Score 15.2; DB 7; Length 28;
	Best Local Similarity 50.0%; Pred. No. 6.8e+03;
	Matches 10; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
QY	5 GUCUCUCCUUUCCGCCACCUC 24
DB	8 GTCTCTCCTTTTCCAGTTC 27
	: : : : : :
RESULT 14	
AAV91451/c	
ID	AAV91451 standard; RNA; 29 BP.
XX	
AC	AAV91451;
XX	
DT	18-FEB-1999 (first entry)
XX	
DE	Human C-raf hammerhead ribozyme nucleotide position 220.
XX	
KW	Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
KW	target; substrate; catalyst; modulation; expression; Raf gene; delivery;
KW	screening; identification; synthesis; deprotection; purification; cancer;
KW	inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
KW	restenosis; rheumatoid arthritis; ss.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	WO9850530-A2.
XX	
PD	12-NOV-1998.
XX	
PF	05-MAY-1998; 98WO-US0009249.
XX	
PR	09-MAY-1997; 97US-0046059P.
PR	09-JUN-1997; 97US-0049002P.
PR	03-JUL-1997; 97US-0051718P.
PR	22-AUG-1997; 97US-0056808P.
PR	02-OCT-1997; 97US-0061321P.
PR	02-OCT-1997; 97US-0061324P.
PR	05-NOV-1997; 97US-0064866P.
PR	19-DEC-1997; 97US-0068212P.
XX	
PA	(RIBO-) RIBOZYME PHARM INC.
XX	
PI	Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
PI	Parry T, Baigelman L, Mcswiggen JA, Karpeisky A, Burgin A;
PI	Thompson J, Workman CT, Beaudry A, Sweedler D;
DR	WPI; 1999-009494/01.
XX	
PT	Identifying new catalytic nucleic acid that modulates selected processes
PT	- especially ribozymes that cleave Raf RNA for treating cancer,
PT	restenosis, and also new ribozymes and modified nucleoside triphosphates
PT	used as antiviral agents and synthons.
XX	
PS	Claim 151; Page 146; 259pp; English.
XX	
CC	A method has been developed for the identification of a nucleic acid

CC capable of modulating a process in a biological system. The method
CC comprises: (a) introducing into the system a random library of nucleic
CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
CC in systems where modulation has occurred and/or determining the sequence
CC of at least part of the SBDs in such systems. Nucleic acid molecules with
CC endonuclease activity and catalytic activity, from the present invention,
CC are used to modulate gene expression in plant and mammalian cells and to
CC cleave target nucleic acid, particularly for treating systemic diseases
CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
CC ascites and infection. They may also be used to detect genetic drift and
CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
CC with RNA-cleaving activity that modulate expression of the Raf gene, are
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
CC generally any condition associated with the level of c-raf. Introduction
CC of sugar/phosphate modifications increases stability against nuclease and
CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
CC method, specifically for modulating the expression of a Raf gene
XX
SQ Sequence 29 BP; 11 A; 3 C; 9 G; 0 T; 5 U; 1 Other;

Query Match 61.7%; Score 14.8; DB 2; Length 29;
Best Local Similarity 47.4%; Pred. No. 1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 6 UCUCUCUUUUGCCACCUC 24
Db 29 TCTCTCCTTTTCGNCTCATC 11

RESULT 15
AAFO1081/c

ID AAF01081 standard; RNA; 29 BP.

XX AC

XX AC

XX 16-FEB-2001 (first entry)

XX Hammerhead ribozyme #1072.

XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;

XX interferon alpha; ss.

XX Homo sapiens.

XX WO200061729-A2.

XX 19-OCT-2000.

XX 11-APR-2000; 2000WO-US009721.

XX 12-APR-1999; 99US-0129390P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, Zwick M, Pavco P, Meswiggen J;

XX WPI; 2000-647423/62.

XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
XX Claim 32; Page 80; 164pp; English.

XX The present invention relates to enzymatic and antisense nucleic acid
XX molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TE-1, the GATA transcription
CC factor gene, IRF-2 and/or the C/EBP Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
XX interferon alpha

XX
SQ Sequence 29 BP; 13 A; 2 C; 9 G; 0 T; 4 U; 1 Other;
Query Match 61.7%; Score 14.8; DB 3; Length 29;
Best Local Similarity 47.4%; Pred. No. 1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 6 UCUCUCUUUUGCCACCUC 24
Db 29 TCTCTCCTTTTCGNCTCATC 11

Search completed: October 16, 2006, 14:16:00
Job time : 126.594 secs

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C 2	15.6	65.0	24	2	AR010025	Sequence
C 3	15.6	65.0	24	2	AR034743	Sequence
C 4	15.6	65.0	24	2	AR034760	Sequence
C 5	15.6	65.0	24	2	124740	Sequence 3
C 6	15.6	65.0	24	2	124752	Sequence 15
C 7	14.8	61.7	29	2	BD253279	Regulator
C 8	14.8	61.7	29	2	AR0265215	Sequence
C 9	14.4	60.0	18	2	AR072296	Sequence
C 10	14.4	60.0	18	2	126407	Sequence 99
C 11	14.2	59.2	21	2	128585	Sequence 38
C 12	14.2	59.2	21	2	158747	Sequence 18
C 13	14.2	59.2	25	2	AX649750	Sequence
C 14	14.2	59.2	25	2	AX649751	Sequence
C 15	14.2	59.2	25	2	AX649752	Sequence
C 16	14.2	59.2	25	2	AX649753	Sequence
C 17	14.2	59.2	25	2	AX649754	Sequence
C 18	14.2	59.2	25	2	AX649755	Sequence

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TITLE      Cloning and expression of PUR protein
JOURNAL    Patent: US 5756684-A 38 26-MAY-1998;
FEATURES   Location/Qualifiers
source     1..24
            /organism="unknown"
            /mol_type="unassigned DNA"
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Query Match      65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 1.9e+04;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy      3 UUGUCUCUCUUCGCCACCUC 24
      :::::|:|:|:|:|:|:|
Db      2 TTTTCTCTCCCTCCACCACCTC 23

RESULT 3
LOCUS      AR034743/c
DEFINITION Sequence 20 from patent US 5869622.
ACCESSION  AR034743
VERSION     AR034743.1 GI:5950348
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 24)
AUTHORS   Johnson,E.M. and Bergemann,A.D.
TITLE     Monoclonal antibodies to the pur protein
JOURNAL   Patent: US 5869622-A 20 09-FEB-1999;
FEATURES   Location/Qualifiers
source     1..24
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            /mol_type="unassigned DNA"
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Query Match      65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 1.9e+04;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy      3 UUGUCUCUCUUCGCCACCUC 24
      :::::|:|:|:|:|:|:|
Db      2 TTTTCTCTCCCTCCACCACCTC 23

RESULT 4
LOCUS      AR034760
DEFINITION Sequence 38 from patent US 5869622.
ACCESSION  AR034760
VERSION     AR034760.1 GI:5950365
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 24)
AUTHORS   Johnson,E.M. and Bergemann,A.D.
TITLE     Monoclonal antibodies to the pur protein
JOURNAL   Patent: US 5869622-A 38 09-FEB-1999;
FEATURES   Location/Qualifiers
source     1..24
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            /mol_type="unassigned DNA"
ORIGIN
Query Match      65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 1.9e+04;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy      3 UUGUCUCUCUUCGCCACCUC 24
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Db      23 TTTTCTCTCCCTCCACCACCTC 2

RESULT 5
LOCUS      I24740/c
DEFINITION Sequence 3 from patent US 5545551.
ACCESSION  I24740
VERSION     I24740.1 GI:1604610
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 24)
AUTHORS   Johnson,E.M. and Bergmann,A.D.
TITLE     Cloning and expression of pur protein
JOURNAL   Patent: US 5545551-A 3 13-AUG-1996;
FEATURES   Location/Qualifiers
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Query Match      65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 1.9e+04;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy      3 UUGUCUCUCUUCGCCACCUC 24
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Db      23 TTTTCTCTCCCTCCACCACCTC 2

RESULT 6
LOCUS      I24752
DEFINITION Sequence 15 from patent US 5545551.
ACCESSION  I24752
VERSION     I24752.1 GI:1604622
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 24)
AUTHORS   Johnson,E.M. and Bergmann,A.D.
TITLE     Cloning and expression of pur protein
JOURNAL   Patent: US 5545551-A 15 13-AUG-1996;
FEATURES   Location/Qualifiers
source     1..24
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            /mol_type="unassigned DNA"
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Query Match      65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 1.9e+04;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy      3 UUGUCUCUCUUCGCCACCUC 24
      :::::|:~|:~|:~|:~|:~|
Db      23 TTTTCTCTCCCTCCACCACCTC 23

RESULT 7
LOCUS      BD253279/c
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION  BD253279
VERSION     BD253279.1 GI:33063049
KEYWORDS   JP 2002541795-A/1072.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 29)
AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE     Regulation of repressor genes using nucleic acid molecules
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ORIGIN
Query Match          59.2%; Score 14.2; DB 2; Length 21;
Best Local Similarity 36.8%; Pred. No. 8.1e+04;
Matches 7; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
QY 1 UAUGUCUCUCUCCUUUCGCC 19
Db 19 TTTATCTCTCCTTTCTCC 1

RESULT 12
I58747/c
LOCUS AX649750/c
DEFINITION Sequence 38 from patent US 5652350.
ACCESSION I58747
VERSION I58747.1 GI:2477985
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Watanabe,K.A., Ren,W.-Y. and Weil,R.
TITLE Complementary DNA and toxins
JOURNAL Patent: US 5652350-A 38 29-JUL-1997;
FEATURES
source
1..21
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ORIGIN
Query Match          59.2%; Score 14.2; DB 2; Length 21;
Best Local Similarity 36.8%; Pred. No. 8.1e+04;
Matches 7; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
QY 1 UAUGUCUCUCUCCUUUCGCC 19
Db 19 TTTATCTCTCCTTTCTCC 1

RESULT 13
AX649750/c
LOCUS AX649750
DEFINITION Sequence 1590 from Patent EP1273660.
ACCESSION AX649750
VERSION AX649750.1 GI:29152568
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Homo sapiens (human)
TITLE Human sodium-hydrogen exchanger like protein 1
JOURNAL Patent: EP 1273660-A 1590 08-JAN-2003;
FEATURES
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ORIGIN
Query Match          59.2%; Score 14.2; DB 2; Length 25;
Best Local Similarity 52.6%; Pred. No. 8.2e+04;
Matches 10; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUUGUCUCUCUCCUUUCGCCA 20
Db 25 ACTGTCCTCCATTCCTCC 7

ORIGIN
Query Match          59.2%; Score 14.2; DB 2; Length 21;
Best Local Similarity 36.8%; Pred. No. 8.1e+04;
Matches 7; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
QY 1 UAUGUCUCUCUCCUUUCGCC 19
Db 19 TTTATCTCTCCTTTCTCC 1

RESULT 14
AX649751/c
LOCUS AX649751
DEFINITION Sequence 1591 from Patent EP1273660.
ACCESSION AX649751
VERSION AX649751.1 GI:29152569
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Gu.Y.
TITLE Human sodium-hydrogen exchanger like protein 1
JOURNAL Patent: EP 1273660-A 1591 08-JAN-2003;
FEATURES
source
1..25
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match          59.2%; Score 14.2; DB 2; Length 25;
Best Local Similarity 52.6%; Pred. No. 8.2e+04;
Matches 10; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUUGUCUCUCUCCUUUCGCCA 20
Db 24 ACTGTCCTCCATTCCTCC 6

RESULT 15
AX649752/c
LOCUS AX649752
DEFINITION Sequence 1592 from Patent EP1273660.
ACCESSION AX649752
VERSION AX649752.1 GI:29152570
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Gu.Y.
TITLE Human sodium-hydrogen exchanger like protein 1
JOURNAL Patent: EP 1273660-A 1592 08-JAN-2003;
FEATURES
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ORIGIN
Query Match          59.2%; Score 14.2; DB 2; Length 25;
Best Local Similarity 52.6%; Pred. No. 8.2e+04;
Matches 10; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUUGUCUCUCUCCUUUCGCCA 20
Db 23 ACTGTCCTCCATTCCTCC 5

Search completed: October 16, 2006, 14:52:15
Job time : 591.797 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:04:23 ; Search time 1032.18 Seconds
(without alignments)
1300.222 Million cell updates/sec

Title: US-10-604-726A-5136
Perfect score: 24
Sequence: 1 uauugucuccuucgccaccu 24
Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 56556

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est3.*
3: gb_est4.*
4: gb_est5.*
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7: gb_est8.*
8: gb_est9.*
9: gb_est10.*
10: gb_est11.*
11: gb_est12.*
12: gb_est13.*
13: gb_est14.*
14: gb_est15.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	13.4	55.8	25	11	AZ775852 2M0009N01
C 2	13.4	55.8	26	3	BQ586604 E012388-0
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C 4	12.8	53.3	29	13	CL983097 GC0336 TI
C 5	12.4	51.7	30	11	AZ604126 IM0423013
C 6	12.2	50.8	24	4	CA850924 D08B11 D2
C 7	12.2	50.8	27	11	AZ340258 IM0072C20
C 8	12.2	50.0	23	11	AZ329650 IM0054A13
C 9	12.2	50.0	23	11	AZ514958 IM0054A13
C 10	12.2	50.0	27	13	CL983109 GC0348 TI
C 11	12.2	50.0	28	11	BH901484 SALK 0796
C 12	11.8	49.2	28	14	AJ545811 Drosophila
C 13	11.6	48.3	21	11	AZ475883 IM0294J14
C 14	11.6	48.3	25	1	AI539240 tp64b08.x
C 15	11.6	48.3	26	1	AZ454352 IM0256G18
C 16	11.6	48.3	28	1	AI183010 ub92e02.r
C 17	11.6	48.3	29	11	AZ780850 2M0018A02
C 18	11.6	48.3	29	11	AZ828692 2M0105N15
C 19	11.4	47.5	27	11	AZ432080 IM0217024

20	11.4	47.5	28	1	AI118404
21	11.4	47.5	28	11	AZ342196
C 22	11.4	47.5	28	14	TA205E06P
23	11.4	47.5	29	11	AZ345594
24	11.4	47.5	29	13	CZ472219
C 25	11.4	47.5	30	13	CZ477542
C 26	11.2	46.7	18	8	CN750241
C 27	11.2	46.7	21	14	AG189071
C 28	11.2	46.7	21	14	AG202804
C 29	11.2	46.7	22	8	CO788412
C 30	11.2	46.7	25	13	CL692271
C 31	11.2	46.7	27	11	AZ416143
C 32	11.2	46.7	27	14	AG198505
C 33	11.2	46.7	28	11	AZ829200
C 34	11.2	46.7	29	12	BZ593222
C 35	11.2	46.7	30	13	CZ175615
C 36	11.2	46.7	19	13	CL671134
C 37	11.2	45.8	22	1	AU014100
C 38	11.2	45.8	22	1	AU014106
C 39	11.2	45.8	22	11	AZ942905
C 40	11.2	45.8	23	14	CT014183
C 41	11.2	45.8	27	14	TA204D03P
C 42	11.2	45.8	30	11	AZ976285
C 43	10.8	45.0	25	1	AI527253
C 44	10.8	45.0	25	11	AZ479489
C 45	10.8	45.0	27	11	AZ949222

ALIGNMENTS

RESULT 1
AZ775852/c
LOCUS
DEFINITION
2M0009N01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0009N01 F, genomic survey sequence.

ACCESSION
AZ775852

VERSION
GSS.

KEYWORDS
SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00

Plate: 0009 row: N column: 01

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 25.

Location/Qualifiers

1..25

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AZ342196 IM0075F07
AL479131 T. brucei
AZ345594 IM0080016
CZ472219 d01414-5p
CZ477542 d11088-5p
CN750241 ADPT-VIII
AG189071 Pan trogl
AG202804 Pan trogl
CO788412 NT004A GO
CL692271 PRI0158C
AZ416143 IM0191G14
AG198505 Pan trogl
AZ829200 2M0106N11
BZ593222 SALK 0682
CZ175615 MIAA-6F19
CL671134 PRI0163d
AU014100 AU014100 -
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AZ942905 2M0203K13
CT014183 KBRH122F2
AL476477 T. brucei
AZ976285 2M0251H09
AI527253 u150807-X
AZ479489 IM0300H08
AZ949222 2M0212A12

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 55.8%; Score 13.4; DB 11; Length 25;
Best Local Similarity 43.5%; Pred. No. 3.3e+05;
Matches 10; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
QY 2 AUGUCUCUCCUUUGCCACCUC 24
|::|::|::|::|::|::|
Db 24 ATTCATCTCCTTTCACACCCC 2

RESULT 2

BQ586604/c
LOCUS
DEFINITION E012388-024-012-E21-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone
024-012-E21 5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

COMMENT

Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mplz-koeln.mpg.de
Insert Length: 26 Std Error: 0.00
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FEATURES

source

1..26
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Matches 11; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
QY 2 AUGUCUCUCCUUUGCCACCUC 24
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Db 23 ATATTCTGCGCTTCTCCGCCCC 1

RESULT 3

AI673609

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

AI673609 28 bp mRNA linear EST 18-DEC-1999
we76d05.xl Soares Dieckgraebe colon.NHCD Homo sapiens cDNA clone
IMAGE:2347017.3, similar to TR:060318 O60318 MCM3 IMPORT FACTOR ;,
mRNA sequence.
AI673609
AI673609.1 GI:4853340
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 28)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgsb@bbs-rmail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 850 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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disease"
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/clone_lib="Soares_Dieckgraebe_colon.NHCD"
/note="Organ: colon; Vector: pT73b-Paci; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
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double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Tissue samples
provided by Dr. Brian Dieckgraebe (Washington University,
dieck@im.wustl.edu); colonic mucosa represents a range of
disease involvement from moderate to severe Crohn's
disease; samples include both perforating (fistulas) and
non-perforating samples. Library constructed by Bento
Soares and M. Fatima Bonaldo."

ORIGIN	Query Match	54.2%;	Score 13;	DB 1;	Length 28;
	Best Local Similarity	38.1%;	Pred. No. 5e+05;		
	Matches	8;	Conservative	8;	Mismatches 5; Indels 0; Gaps 0;
Qy	1	UAUUGUCUCCUUCGCCAC 21			
	8	TCTGTTCTCTCTTCTCCAC 28			
Db					
RESULT 4	CL983097/c				
	LOCUS	29 bp	mRNA	linear	GSS 21-SEP-2004
	DEFINITION	GC0336 TIGEM gene trap library Mus musculus cDNA clone 10662.60,			
ACCESSION	CL983097				
	VERSION	CL983097.1	GI:52420677		
	KEYWORDS				
SOURCE	Mus musculus	(house mouse)			
	ORGANISM				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
REFERENCE	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;				
	Sciurognathi; Muridea; Muridae; Murinae; Mus.				
	1 (bases 1 to 29)				
AUTHORS	Cobellis, G., Nicolaus, G., Iovino, M., Romito, A., Marra, E.,				
	Barbarisi, M., Sardiello, M., Di Giorgio, F.P., Iovino, N., Zollo, M.,				
	Ballabio, A. and Cortese, R.				
TITLE	Tagging genes with cassette-exchange sites				
	Nucleic Acids Res. 33 (4), e44 (2005)				
	15741177				
JOURNAL	PubMed				
	COMMENT	Contact: TIGEM			
	107				
FEATURES	TIGEM				
	Location/Qualifiers				
	1..29				
source	/organism="Mus musculus"				
	/mol_type="mRNA"				
	/strain="129 Ola"				
Qy	8	UCUCCUUUGGCCACCUC 24			
	21	TCGCCATTGCCCANCTC 5			
Db					
RESULT 5	AZ604126/c				
	LOCUS	30 bp	DNA	linear	GSS 13-DEC-2000
	DEFINITION	IM0423013R Mouse 10kb plasmid UUGC1M library Mus musculus genomic			
ACCESSION	AZ604126				
	VERSION	clone UUGC1M0423013 R, genomic survey sequence.			
	1				
ORIGIN	Query Match	53.3%;	Score 12.8;	DB 13;	Length 29;
	Best Local Similarity	58.8%;	Pred. No. 6.2e+05;		
	Matches	10;	Conservative	4;	Mismatches 3; Indels 0; Gaps 0;
Qy	8	UCUCCUUUGGCCACCUC 24			
	21	TCGCCATTGCCCANCTC 5			
Db					
ORIGIN	Query Match	51.7%;	Score 12.4;	DB 11;	Length 30;
	Best Local Similarity	40.9%;	Pred. No. 9.3e+05;		
	Matches	9;	Conservative	7;	Mismatches 6; Indels 0; Gaps 0;
Qy	3	UUGUCUCCUUCGCCACCUC 24			
	28	TTGCCTCACCITTCCTCTCTC 7			
Db					
RESULT 6	CA850924				
	LOCUS	24 bp	mRNA	linear	EST 01-AUG-2003
	DEFINITION	D08B11.D23 04.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max			
ACCESSION	CA850924				
	VERSION	CDNA clone D08B11 5', mRNA sequence.			
	1				

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 30)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Becorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Genome Center

Rm. 308, Biomedical

Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000

Std Error: 0.00

Plate: 0423

row: O

column: 13

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 30.

Location/Qualifiers

1..30

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0423013"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match

Best Local Similarity

Matches

9;

Conservative

7;

Mismatches

6;

Indels

0;

Gaps

0;

Qy

28

TTGCCTCACCITTCCTCTCTC 7

Db

RESULT 6

CA850924

LOCUS

DEFINITION

ACCESSION

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0054 row: A column: 13
 Seq primer: CACACAGAAACACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers

FEATURES

source
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0054A13"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 50.0%; Score 12; DB 11; Length 23;
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 UAUUGUCUCUCC 12
 :|:|:|:|:|:
 Db 11 TATTGTCCTCC 22

RESULT 9

AZ514958
 LOCUS
 DEFINITION 1M0054A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0054A13 F, genomic survey sequence.
 AZ514958
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 23)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0054 row: A column: 13
 Seq primer: CGTTGTAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers

FEATURES

source
 1. .23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0054A13"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 50.0%; Score 12; DB 11; Length 23;
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 UAUUGUCUCUCC 12
 :|:|:|:|:|:
 Db 11 TATTGTCCTCC 22

RESULT 10

CL983109/c
 LOCUS
 DEFINITION GC0348 TIGEM gene trap library Mus musculus cDNA clone 10863.13, mRNA sequence.
 CL983109
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 27)
 Cobellis, G., Niclaus, G., Iovino, M., Romito, A., Marra, E., Barbarisi, M., Sardiello, M., Di Giorgio, F. P., Iovino, N., Zollo, M., Ballabio, A. and Cortese, R.
 Tagging genes with cassette-exchange sites
 Nucleic Acids Res. 33 (4), e44 (2005)
 15741177
 Contact: TIGEM
 107
 TIGEM
 Via P. Castellino, 111, 80131 NAPOLI, ITALY
 Tel: +390816132205

Fax: +390815790919
Email: cobellis@gem.it
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from TIGEM. Annotation information available from TIGEM
Class: Gene Trap.

FEATURES

```

1. 27
/organism="Mus musculus"
/mol_type="mRNA"
/strains="129 Ola"
/db_xref="taxon:10090"
/clone="10863.13"
/sex="male"
/cell_type="Embryonic stem cell"
/cell_line="E14"
/clone_lib="TIGEM gene trap library"
/note="Vector: pBIP1"

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ORIGIN

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Query Match      50.0%; Score 12; DB 13; Length 27;
Best Local Similarity 55.0%; Pred.No. 1.4e+06;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      5  GUCUCUCUUCUUGCCACCUC 24
      |||::|::|::|::|::|
Db      23  GGCTCTCACTCCGCCAGCTC 4

```

RESULT 11

BH901484	BH901484	28 bp	DNA	linear	GSS 04-SEP-2002
LOCUS	SALK_079650.53.10.x Arabidopsis thaliana	TDNA insertion lines			
DEFINITION	Arabidopsis thaliana genomic clone SALK_079650.53.10.x, genomic survey sequence.				
ACCESSION	BH901484				
VERSION	BH901484.1	GI:22712365			
KEYWORDS	GSS.				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
	1. (bases 1 to 28)				
REFERENCE	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,				
AUTHORS	Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.				

TITLE

JOURNAL
COMMENT

Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.

FEATURES

```

1. 28
source
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_079650.53.10.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at

```

the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

```

Query Match      50.0%; Score 12; DB 11; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 UAUUGUCUCUCUUCGCGCA 20
   : : : : : : : : : :
Db 5 TTTTTCCTCCTGCACCA 24

```

RESULT 12

DM545811/c	DM545811	28 bp	DNA	linear	GSS 24-FEB-2003
LOCUS					
DEFINITION	Drosophila melanogaster flanking sequence of RS P element insertion P[RS]CB-6297-3, clone library P[RS3], genomic survey sequence.				
ACCESSION	AJ545811.1				
VERSION	GI:28553693				
KEYWORDS	GSS; genome survey sequence.				
SOURCE	Drosophila melanogaster (fruit fly)				
ORGANISM	Drosophila melanogaster				
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
REFERENCE	1				
AUTHORS	Ryder, E.-J., Ashburner, M., Bagunya, J., Blows, F., Bucheton, A.,				

TITLE

JOURNAL	the Drosdel second generation deficiency kit
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 28)
TITLE	Ryder, E.J.
JOURNAL	Direct Submission
COMMENT	Submitted (17-FEB-2003) Ryder E.J., Department of Genetics, University of Cambridge, Downing Street, CB2 3EH, UNITED KINGDOM The insertion point of the p element is before base 1 of the sequence. Further information about this p element insertion line can be found at http://www.flyseq.org.uk and http://www.drosdel.org.uk .

FEATURES

```

source
1. .28
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/chromosome="3L"
/clone="P{RS3}CB-6297-3"
/clone_lib="P{RS3}"
/notes="read-5', end"
1. .28
/misc_feature
/notes="P element insertion in the 5' to 3' orientation"

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ORIGIN

Query Match	49.2%;	Score 11.8;	DB 14;	Length 28;
Best Local Similarity	60.0%;	Pred. No. 1.7e+06;		
Matches	9;	Conservative	4;	Mismatches 2;
Indels				0;
Gaps				0;
Qy	7	CUCUCCUUNCGCCAC	21	
		: : : : : :		
Db	25	CTCTCTCTGCGCAC	11	

RESULT 13

AZ475883/c
LOCUS
AZ475883 21 bp DNA linear GSS 04-OCT-2000
DEFINITION
IM0294J14.F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0294J14.F, genomic survey sequence.
ACCESSION
AZ475883

```

VERSION      AZ475883.1  GI:10634008
KEYWORDS     Mus musculus (house mouse)
SOURCE       Mus musculus
ORGANISM     Mus musculus

REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0294 row: J column: 14
              Seq primer: CGTTGTAACGACGCCAGT
              Class: plasmid ends
              High quality sequence stop: 21.

FEATURES     Location/Qualifiers
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             /organism="Mus musculus"
             /mol_type="genomic DNA"
             /strain="C57BL/6J"
             /db_xref="taxon:10090"
             /clone="UUGCLM0294J14"
             /sex="Male"
             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
             /clone_lib="Mouse 10kb plasmid UUGCLM library"
             /notes="Vector: PWD42nv; Purified genomic DNA from M.
             musculus C57BL/6J (male) was obtained from the Jackson
             Laboratory Mouse DNA Resource
             (http://www.jax.org/resources/documents/dnares/). The DNA
             was hydrodynamically sheared by repeated passage through a
             0.005 inch orifice at constant velocity. The sheared DNA
             was blunt end-repaired with T4 DNA polymerase and T4
             polynucleotide kinase. Adaptor oligonucleotides were
             ligated to the blunt ends in high molar excess. The
             adaptor DNA was purified and size-selected for a 9.5 to
             10.5 kb range using preparative agarose gel.
             10.5 kb range using preparative agarose gel.
             electrophoresis. Vector DNA was prepared from a derivative
             of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
             inducible derivative of plasmid R1. The vector was ligated
             with adaptors complementary to the insert adaptors and
             purified. The sheared, adaptor mouse DNA was annealed to
             adaptor vector DNA, and transformed into
             chemically-competent E. coli XL10-Gold (Stratagene) cells
             and selected for ampicillin resistance."

ORIGIN
Query Match      48.3%; Score 11.6; DB 11; Length 21;
Best Local Similarity 44.4%; Pred. No. 2e+06;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 7 CUUCUCCUUGCCACCUC 24
Db 21 CTTCTCTTCTTCCCTTC 4

RESULT 14
A1539240/c
LOCUS
DEFINITION      tp64b08.x1 NCI_CGAP Ut3 Homo sapiens cDNA clone IMAGE:2204055 3'
                 similar to TR:Q40726 Q40726 DNA BINDING PROTEIN ;, mRNA sequence.

ACCESSION      A1539240
VERSION        A1539240.1  GI:4453375
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1192 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No.

FEATURES     Location/Qualifiers
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             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:2204055"
             /tissue_type="poorly-differentiated endometrial
             adenocarcinoma, 2 pooled tumors"
             /lab_host="DH10B"
             /clone_lib="NCI CGAP Ut3"
             /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
             Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
             Average insert size 1.45 kb. Life Technologies catalog #:
             11541-018"

ORIGIN
Query Match      48.3%; Score 11.6; DB 1; Length 25;
Best Local Similarity 44.4%; Pred. No. 2e+06;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 6 UCUCUCCUUCUCCACCUC 23
Db 25 TTTCCCTTCTCCCTCCT 8

RESULT 15
AZ454352
LOCUS
DEFINITION      1M0256G18F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
                 clone UUGCLM0256G18 F, genomic survey sequence.

ACCESSION      AZ454352
VERSION        AZ454352.1  GI:10612477
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb

```

**JOURNAL
COMMENT**

plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000
 Plate: 0256 row: G column: 18
 Seq primer: CGTTGTAACAGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 26.

FEATURES

source

ORIGIN

```
Query Match          48.3%; Score 11.6; DB 11; Length 26;
Best Local Similarity 50.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
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Search completed: October 16, 2006, 15:51:29
Job time : 1035.18 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:11:03 ; Search time 55.5789 Seconds
(without alignments)
807.979 Million cell updates/sec

Title: US-10-604-726A-5136

Perfect score: 24

Sequence: 1 uauugucuccuucgcaccuc 24

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 1097684

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1 COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5 COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.6	65.0	24	2	US-08-014-943A-3
C 2	15.6	65.0	24	2	US-08-014-943A-15
C 3	15.6	65.0	24	2	US-08-486-421-20
C 4	15.6	65.0	24	2	US-08-486-421-38
C 5	15.6	65.0	24	2	US-08-470-911-20
C 6	15.6	65.0	24	2	US-08-470-911-38
C 7	15.6	65.0	24	2	US-08-486-809-20
C 8	15.6	65.0	24	2	US-08-486-809-38
C 9	14.8	61.7	29	3	US-07-672-530C-16
C 10	14.4	60.0	18	2	US-07-977-284A-99
C 11	14.4	60.0	18	2	US-08-256-426B-99
C 12	14.2	59.2	21	2	US-08-242-664-38
C 13	14.2	59.2	21	2	US-08-484-138-38
C 14	14.2	59.2	21	7	PCT-US95-06379-38
C 15	14	58.3	24	2	US-08-014-943A-12
C 16	14	58.3	24	2	US-08-486-421-34
C 17	14	58.3	24	2	US-08-470-911-34
C 18	14	58.3	24	2	US-08-486-809-34
C 19	14	58.3	25	3	US-09-396-196G-81941
C 20	13.8	57.5	20	3	US-09-118-408-10
C 21	13.8	57.5	20	3	US-09-506-855-10
C 22	13.8	57.5	20	3	US-09-311-178B-10
C 23	13.8	57.5	20	3	US-09-619-740-10

C 24	13.8	57.5	20	3	US-09-198-452A-3360	Sequence 3360, Ap
C 25	13.8	57.5	20	3	US-09-506-852-10	Sequence 10, Appl
C 26	13.8	57.5	20	3	US-10-392-705-10	Sequence 10, Appl
C 27	13.6	56.7	25	3	US-09-396-196G-64399	Sequence 64399, A
C 28	13.6	56.7	25	3	US-09-396-196G-119671	Sequence 119671, A
C 29	13.4	55.8	17	2	US-07-977-284A-100	Sequence 100, App
C 30	13.4	55.8	17	2	US-08-256-426B-100	Sequence 100, App
C 31	13.4	55.8	24	3	US-08-445-463B-56	Sequence 56, Appl
C 32	13.4	55.8	24	3	US-08-445-463B-57	Sequence 56, Appl
C 33	13.4	55.8	24	3	US-08-445-464C-56	Sequence 57, Appl
C 34	13.4	55.8	24	3	US-08-445-464C-57	Sequence 57, Appl
C 35	13.4	55.8	24	3	US-08-044-857D-56	Sequence 56, Appl
C 36	13.4	55.8	24	3	US-08-044-857D-57	Sequence 57, Appl
C 37	13.4	55.8	24	7	PCT-US94-03437-56	Sequence 56, Appl
C 38	13.4	55.8	24	7	PCT-US94-03437-57	Sequence 57, Appl
C 39	13.4	55.8	25	3	US-09-544-398B-365	Sequence 365, App
C 40	13.4	55.8	25	3	US-09-543-771B-365	Sequence 365, App
C 41	13.4	55.8	25	3	US-09-396-196G-14417	Sequence 14417, A
C 42	13.4	55.8	25	3	US-09-396-196G-14428	Sequence 14428, A
C 43	13.4	55.8	25	3	US-09-396-196G-57430	Sequence 57430, A
C 44	13.4	55.8	25	3	US-09-396-196G-117149	Sequence 117149, A
C 45	13.4	55.8	28	3	US-09-175-928B-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-08-014-943A-3/c
; Sequence 3, Application US/08014943A
; Patent No. 5545551
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergmann, Andrew D.
; TITLE OF INVENTION: Cloning And Expression Of PUR Protein
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,943A
; FILING DATE: 02/FEB/1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; US-08-014-943A-3

Query Match 65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 6.4e+02;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 UUGUCUCUCCUUUCGCCACCUC 24
:::|:|:|:|:|:|:|
DG 23 TTTTCTCTCCCCTCCACCACTC 2

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RESULT 2
US-08-014-943A-15
; Sequence 15, Application US/08014943A
; Patent No. 5545551
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: Cloning And Expression Of PUR Protein
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,943A
; FILING DATE: 02/FEB/1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-014-943A-15

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Query Match      65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 6.4e+02;
Matches 11: Conservative 7; Mismatches 4; Indels 0; Gaps 0;
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RECORD 3
US-08-486-421-20/c
; Sequence 20, Application US/08486421
; Patent No. 5672479
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,421
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,911
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; US-08-486-421-20
; Query Match 65.0%; Score 15.6; DB 2; Length 24;
; Best Local Similarity 50.0%; Pred. No. 6.4e+02;
; Matches 11; Conservative 7; Mismatches 4; Indels

QY      3 UUGUCUCUCCUUGGCCACCUC 24
        ::|||::|||||
Db       23 TTTCCTCCTCCACCACCTC 2
        :|||::|||::|

RESULT 4
US-08-486-421-38
; Sequence 38, Application US/08486421
; Patent No. 5672479
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,421
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,911
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE

```

; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-486-421-38

Query Match 65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 6.4e+02;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 UUGUCUCUCCUUGCCACCUC 24
Db 2 TTTTCTCTCCCTCCACCCTC 23

RESULT 5

US-08-470-911-20/c
; Sequence 20, Application US/08470911
; Patent No. 5756684
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,911
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 20:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-470-911-20

Query Match 65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 6.4e+02;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 UUGUCUCUCCUUGCCACCUC 24
Db 23 TTTTCTCTCCCTCCACCCTC 2

RESULT 6

US-08-470-911-38
; Sequence 38, Application US/08470911
; Patent No. 5756684

; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,911
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-470-911-38

Query Match 65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 6.4e+02;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 UUGUCUCUCCUUGCCACCUC 24
Db 2 TTTTCTCTCCCTCCACCCTC 23

RESULT 7

US-08-486-809-20/c
; Sequence 20, Application US/08486809
; Patent No. 5869622
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,809
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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/ APPLICATION NUMBER: US 08/470,911
/ FILING DATE: 06-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/   NAME: Coruzzi, Laura A.
/   REGISTRATION NUMBER: 30,742
/   REFERENCE/DOCKET NUMBER: 6923-053
/ TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (212) 790-9090
/   TELEFAX: (212) 869-9741/8864
/   TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 24 base pairs
/   TYPE: nucleic acid
/   STRANDEDNESS: single
/   TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
US-08-486-809-20

Query Match      65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 6.4e+02;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY      3 UUGUCUCUCCUUCGCGCACCCUC 24
Db      23 TTTTCTCTCCTCCACCCACCTC 2

RESULT 8
US-08-486-809-38
/ Sequence 38, Application US/08486809
/ Patent No. 5869622
/ GENERAL INFORMATION:
/   APPLICANT: Johnson, Edward M.
/   APPLICANT: Bergemann, Andrew D.
/   TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
/   NUMBER OF SEQUENCES: 51
/ CORRESPONDENCE ADDRESS:
/   ADDRESSEE: Pennie & Edmonds
/   STREET: 1155 Avenue of the Americas
/   CITY: New York
/   STATE: New York
/   COUNTRY: U.S.A.
/   ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/   MEDIUM TYPE: Floppy disk
/   COMPUTER: IBM PC compatible
/   OPERATING SYSTEM: PC-DOS/MS-DOS
/   SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/08/486,809
/   FILING DATE: 07-JUN-1995
/   CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: US 08/470,911
/   FILING DATE: 06-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/   NAME: Coruzzi, Laura A.
/   REGISTRATION NUMBER: 30,742
/   REFERENCE/DOCKET NUMBER: 6923-053
/ TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (212) 790-9090
/   TELEFAX: (212) 869-9741/8864
/   TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 38:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 24 base pairs
/   TYPE: nucleic acid
/   STRANDEDNESS: single
/   TOPOLOGY: linear
/ MOLECULE TYPE: DNA
US-08-486-809-38
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Query Match      65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 6.4e+02;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY      3 UUGUCUCUCCUUCGCGCACCCUC 24
Db      2 TTTTCTCTCCTCCACCCACCTC 23

RESULT 9
US-07-672-530C-16/c
/ Sequence 16, Application US/07672530C
/ Patent No. 6492137
/ GENERAL INFORMATION:
/   APPLICANT: SUCOV, HENRY M
/   APPLICANT: EVANS, RONALD M
/   APPLICANT: UMESONO, KAZUHIKO
/   TITLE OF INVENTION: RESPONSE ELEMENT COMPOSITIONS AND ASSAYS EMPLOYING SAME
/   FILE REFERENCE: 088802/1552
/   CURRENT APPLICATION NUMBER: US/07/672,530C
/   CURRENT FILING DATE: 1991-03-19
/   PRIOR APPLICATION NUMBER: 07/438,757
/   PRIOR FILING DATE: 1989-11-16
/   NUMBER OF SEQ ID NOS: 51
/   SOFTWARE: PatentIn Ver. 2.1
/   SEQ ID NO 16
/   LENGTH: 29
/   TYPE: DNA
/   ORGANISM: Artificial Sequence
/   FEATURE:
/   OTHER INFORMATION: Description of Artificial Sequence:
/   OTHER INFORMATION: Oligonucleotide, M2
US-07-672-530C-16

Query Match      61.7%; Score 14.8; DB 3; Length 29;
Best Local Similarity 55.6%; Pred. No. 1.5e+03;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY      7 CUUCUUCUUCGCGCACCCUC 24
Db      23 CTGCTCTTCGTCACCTC 6

RESULT 10
US-07-977-284A-99
/ Sequence 99, Application US/07977284A
/ Patent No. 5558988
/ GENERAL INFORMATION:
/   APPLICANT: Prockop, Darwin J.
/   APPLICANT: Ala-Kokko, Leena
/   APPLICANT: Williams, Charlene J.
/   APPLICANT: Ritvaniemi, Pertti
/   APPLICANT: Baldwin, Clinton
/   APPLICANT: Hopkinson, Ian
/   APPLICANT: Ahmad, Nilofer Nina
/   TITLE OF INVENTION: METHODS OF DETECTING A GENETIC
/   TITLE OF INVENTION: PREDISPOSITION FOR OSTEOARTHRITIS
/   NUMBER OF SEQUENCES: 261
/ CORRESPONDENCE ADDRESS:
/   ADDRESSEE: Woodcock, Waehburn, Kurtz, Mackiewicz & No. 5558988r18
/   STREET: One Liberty Place, 46th floor
/   CITY: Philadelphia
/   STATE: PA
/   COUNTRY: USA
/   ZIP: 19103
/ COMPUTER READABLE FORM:
/   MEDIUM TYPE: Floppy disk
/   COMPUTER: IBM PC compatible
/   OPERATING SYSTEM: PC-DOS/MS-DOS
/   SOFTWARE: WordPerfect 5.1
/ CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/07/977,284A
/   FILING DATE: 13-NOV-1992
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/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: DeLuca, Mark
/ REGISTRATION NUMBER: 33,229
/ REFERENCE/DOCKET NUMBER: TJU-0697
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-3100
/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 99:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: SINGLE
/ TOPOLOGY: LINEAR
/ ANTI-SENSE: NO
/
US-07-977-284A-99

Query Match 60.0%; Score 14.4; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 2.1e+03;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 9 CUCCUUUCCGACCUC 24
Db 3 CTCCTTTCCGACCTC 18

RESULT 11
US-08-256-426B-99
; Sequence 99, Application US/08256426B
; Patent No. 5948611
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Als-Kokko, Leena
; APPLICANT: Williams, Charlene J.
; APPLICANT: Ritvaniemi, Pertti
; APPLICANT: Baldwin, Clinton
; APPLICANT: Hopkinson, Ian
; APPLICANT: Ahmad, Nilofer Nina
; TITLE OF INVENTION: Methods of Detecting A Genetic
; NUMBER OF SEQUENCES: 293
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5948611ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,426B
; FILING DATE: 03-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10964
; FILING DATE: 12-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,284
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark DeLuca
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 99:

/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: SINGLE
/ TOPOLOGY: LINEAR
/ ANTI-SENSE: NO
/
US-08-256-426B-99

Query Match 60.0%; Score 14.4; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 2.1e+03;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 9 CUCCUUUCCGACCUC 24
Db 3 CTCCTTTCCGACCTC 18

RESULT 12
US-08-242-664-38/c
; Sequence 38, Application US/08242664
; Patent No. 5571937
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; APPLICANT: Well, Roger
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/242,664
; FILING DATE: May 12, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
/
US-08-242-664-38

Query Match 59.2%; Score 14.2; DB 2; Length 21;
Best Local Similarity 36.8%; Pred. No. 2.7e+03;
Matches 7; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 1 UAUUGUCUCUCCUUGGCC 19
Db 19 TTTTATCTCTCTCTTCTCC 1

RESULT 13
US-08-484-138-38/c
; Sequence 38, Application US/08484138
; Patent No. 5652350
; GENERAL INFORMATION:
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; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; APPLICANT: Weil, Roger
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44mb
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,138
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683-Z/JPW/MJG
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-484-138-38

Query Match          59.2%; Score 14.2; DB 2; Length 21;
Best Local Similarity 36.8%; Pred. No. 2.7e+03;
Matches 7; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY      1 UAUUGUCUCUCUUCGCGC 19
Db      19 TTTTATCTCTCCCTTCTCC 1

RESULT 14
PCT-US95-06379-38/c
; Sequence 38, Application PC/TUS9506379
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; APPLICANT: Weil, Roger
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44mb
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06379
; FILING DATE: May 13, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
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; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US95-06379-38

Query Match          59.2%; Score 14.2; DB 7; Length 21;
Best Local Similarity 36.8%; Pred. No. 2.7e+03;
Matches 7; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY      1 UAUUGUCUCUCUUCGCGC 19
Db      19 TTTTATCTCTCCCTTCTCC 1

RESULT 15
US-08-014-943A-12/c
; Sequence 12, Application US/08014943A
; Patent No. 5545551
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: Cloning And Expression Of PUR Protein
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,943A
; FILING DATE: 02/FEB/1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; US-08-014-943A-12

Query Match          58.3%; Score 14; DB 2; Length 24;
Best Local Similarity 40.9%; Pred. No. 3.4e+03;
Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY      3 UUGUCUCUCUUCGCGCACCC 24
Db      23 TTTTCTCTTTTCCACCCCTC 2
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Search completed: October 16, 2006, 14:47:14
Job time : 56.5789 secs

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Query Match 66.7%; Score 16; DB 10; Length 25;
Best Local Similarity 45.8%; Pred. No. 4.5e+03;
Matches 11: Conservative 8; Mismatches 5; Indels

Query Match	66.7%	Score 16;	DB 10;	Length 25;
Best Local Similarity	45.8%	Pred. No. 4.5e+03;		
Matches 11: Conservative	8;	Mismatches 5;	Indels 0;	Gaps 0;

	; TITLE OF INVENTION:	Target Genes
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; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47788
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-47788

Query Match          66.7%; Score 16; DB 13; Length 25;
Best Local Similarity 45.8%; Pred.No. 4.5e+03;
Matches 11; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY      1 UAUGUCUCUCCUUUGCGCACCU 24
       :|: |:||::|||:|
Db       25 TATCTCCCTCTTTCACATC 2

RESULT 8
US-10-310-914A-205339
; Sequence 205339, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 205339
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-205339

Query Match          65.8%; Score 15.8; DB 11; Length 24;
Best Local Similarity 89.5%; Pred.No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 AUGUCUCUCCUUUGGCCA 20
       ||| |||||||||
Db       5 AUGUCUCUCCUUUCCCCA 23

RESULT 9
US-11-136-527-276878
; Sequence 276878, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 276878
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-276878

Query Match          65.8%; Score 15.8; DB 16; Length 25;
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; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 35846
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-35846

Query Match      65.0%; Score 15.6; DB 13; Length 25;
Best Local Similarity 40.9%; Pred. No. 6.7e+03;
Matches 9; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY      2 AUGUCUCUCCUUUCCGCCACCU 23
       |:::|::|::|::|::|::|::|
Db      2 ATTCTGCTCCTTGCTACCT 23

RESULT 13
US-10-310-914A-498782
; Sequence 498782, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac.
; APPLICANT: Shiller, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 498782
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-498782

Query Match      64.2%; Score 15.4; DB 11; Length 20;
Best Local Similarity 94.1%; Pred. No. 8.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 UCUCUCCUUUCCGCCACC 22
       |||||
Db      3 UCUCUCCUUUCCGCCCC 19

RESULT 14
US-10-956-157-21624/c
; Sequence 21624, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21624
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
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US-10-956-157-21624

Query Match      64.2%; Score 15.4; DB 10; Length 25;
Best Local Similarity 47.1%; Pred. No. 8.2e+03;
Matches 8; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY      2 AUUGUCUCUCCUUUCCGC 18
       |:::|::|::|::|::|
Db      23 ATTGTCCTCCTTTCTC 7

RESULT 15
US-10-956-157-21630/c
; Sequence 21630, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21630
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-21630

Query Match      64.2%; Score 15.4; DB 10; Length 25;
Best Local Similarity 47.1%; Pred. No. 8.2e+03;
Matches 8; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY      2 AUUGUCUCUCCUUUCCGC 18
       |:::|::|::|::|::|
Db      22 ATTGTCCTCCTTTCTC 6

Search completed: October 16, 2006, 16:22:43
Job time : 338.985 secs
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Query Match	59.2%	Score	14.2;	DB	9;	Length	25;
Best Local Similarity	47.4%	Pred. No.	3.1e+03;				
Matches	9;	Conservative	7;	Mismatches	3;	Indels	0;
Gaps	0;						

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RESULT 9
US-11-348-413-485166/c
; Sequence 485166, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmssted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 485166
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe

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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 14491; WAN01UQID; Start 1352; Stop 1376;
; OTHER INFORMATION: 00000000001000
US-11-348-413-485166

Query Match          59.2%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 3.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 4 UGUCUCUCUUCGCCACC 22
Db 25 TGTCTTTCCTTTAACCACC 7

RESULT 10
US-11-348-413-485167/c
; Sequence 485167, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; OTHER INFORMATION: SEQ ID NO: 14491; WAN01UQID; Start 1353; Stop 1377;
; OTHER INFORMATION: 000000000001000
US-11-348-413-485167

Query Match          59.2%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 3.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 4 UGUCUCUCUUCGCCACC 22
Db 24 TGTCTTTCCTTTAACCACC 6

RESULT 11
US-11-348-413-485168/c
; Sequence 485168, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
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; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 485168
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 14491; WAN01UQID; Start 1354; Stop 1378;
; OTHER INFORMATION: 00000000001000
US-11-348-413-485168

Query Match          59.2%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 3.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 4 UGUCUCUCUUCGCCACC 22
Db 23 TGTCTTTCCTTTAACCACC 5

RESULT 12
US-11-348-413-485634/c
; Sequence 485634, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 485634
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 14505; WAN01UQIX; Start 1590; Stop 1614;
; OTHER INFORMATION: 00000000010000
US-11-348-413-485634

Query Match          59.2%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 3.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUUGUCUCUCUUCGCCCA 20
Db 25 AGTGTCTCTCTTCTTCCA 7

RESULT 13
US-11-348-413-485635/c
; Sequence 485635, Application US/11348413
; Publication No. US20060160121A1
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; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; PRIOR FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 485635
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 14505; WAN01UQIX; Start 1592; Stop 1616;
; OTHER INFORMATION: 00000000010000
US-11-348-413-485635

Query Match          59.2%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 3.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY      2 AUGUGUCUCUCUUGGCCA 20
Db      23 AGTGTCTCTTCTTTCCCA 5
      |.:|.:|.:|.:|.:|
RESULT 14
US-11-348-413-689385/c
; Sequence 689385, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 689385
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 2332; WAN01UMKM_at; Start 686; Stop 710;
; OTHER INFORMATION: 111111100000000
US-11-348-413-689385

Query Match          59.2%; Score 14.2; DB 9; Length 25;
Best Local Similarity 36.8%; Pred. No. 3.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

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Matches 7; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY      1 UAUGUGUCUCUCUUGGCC 19
Db      21 TATTGCTTTTCTTTTACC 3
      |.:|.:|.:|.:|.:|
RESULT 15
US-11-348-413-861056/c
; Sequence 861056, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 861056
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 7205; WAN01UM2G_at; Start 114; Stop 138;
; OTHER INFORMATION: 000000001100000
US-11-348-413-861056

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Job time : 53.2331 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 13:57:30 ; Search time 2092.41 Seconds
(without alignments)
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Title: US-10-604-726A-6033

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Gapop 10_0 , Gapext 1.0

Searched: 636136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 1796954

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 8: gb_sy.*
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- 10: gb_vi.*
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- 12: gb_htg.*
- 13: gb_in.*
- 14: gb_om.*
- 15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	15.8	18.6	24	2	AX443910 Sequence
5	15.8	18.6	25	2	AX447886 Sequence
6	15.4	18.1	28	2	AR770823 Sequence
7	15.4	18.1	28	2	AX234378 Sequence
8	15.4	18.1	30	2	AR004751 Sequence
9	15.4	18.1	30	2	AR008237 Sequence
10	15.4	18.1	30	2	AR137020 Sequence
11	15.4	18.1	30	2	BD105661 Genes sen
12	15.4	18.1	30	2	I77021 Sequence 81
13	15.4	18.1	30	2	I81016 Sequence 81
14	15.4	18.1	30	2	I81112 Sequence 81
15	15.2	17.9	21	2	CS226910 Sequence
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18	15	17.6	17	2	AX215298 Sequence

C 19	15	17.6	17	2	AX215299	Sequence
C 20	15	17.6	17	2	AX215300	Sequence
C 21	15	17.6	24	2	AR080081	Sequence
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C 23	15	17.6	26	2	E08992	PCR primer.
C 24	15	17.6	26	2	I32528	Sequence 48
C 25	15	17.6	26	2	I43473	Sequence 48
C 26	15	17.6	26	2	AR181963	Sequence
C 27	15	17.6	26	2	AR494659	Sequence
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C 34	14.8	17.4	22	2	AR032177	Sequence
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C 36	14.8	17.4	22	2	AR309121	Sequence
C 37	14.8	17.4	22	2	AR372695	Sequence
C 38	14.8	17.4	27	2	AR015990	Sequence
C 39	14.8	17.4	27	2	AR082031	Sequence
40	14.8	17.4	29	2	AR061363	Sequence
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42	14.8	17.4	29	2	AR170337	Sequence
43	14.8	17.4	29	2	I16219	Sequence 45
44	14.8	17.4	29	2	AR263223	Sequence
45	14.8	17.4	29	2	I66705	Sequence 45

ALIGNMENTS

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LOCUS AX399122 26 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 70 from Patent WO0194416.
ACCESSION AX399122
VERSION AX399122.1 GI:21261470
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Majumder, K., Spytek, K.A., Tchernev, V.T., Colman, S.D., Padigar, M., Zerkhusen, B., Gusev, V., Burgess, C., Li, L., Malyankar, U.M., Gangolli, E., Stone, D., Macdougall, J., Smithson, G. and Ellerman, K.
TITLE Novel proteins and nucleic acids encoding same
JOURNAL Patent: WO 0194416-A 70 13-DEC-2001;
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source Curagen Corporation (US)
location/Qualifiers
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LOCUS					
DEFINITION					
ACCESSION					
VERSION					

[illegible]

1 (bases 1 to 30)
Skolnick, M.H., Goldgar, D.E., Miki, Y., Swenson, J., Kamb, A.,

Best Local Similarity 36.0%; Pred. No. 2.6e+06;					
Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;					
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DEFINITION	Genes sensitive to 17q-chained breast cancer and ovarian cancer.				
ACCESSION	BD105661				
VERSION	BD105661.1	GI:22651235			
KEYWORDS	JP 2001346593-A/79.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 30) Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A., Harshman,K.D., Eidens,D.M.S., Tavtigian,S.V., Wiseman,R.W. and Futreal,A.P. Genes sensitive to 17q-chained breast cancer and ovarian cancer Patent: JP 2001346593-A 79 18-DEC-2001; MYRIAD GENETICS INC,UNIVERSITY OF UTAH RESEARCH FOUNDATION, THE UNITED STATES OF AMERICA OS Homo sapiens (human) PN JP 2001346593-A/79 PD 18-DEC-2001 PF 18-APR-2001 JP 2001119644 PR 12-AUG-1994 US 08/289221,02-SEP-1994 US 08/300266 PR 16-SEP-1994 US 08/308104,29-NOV-1994 US 08/348824 PR 24-MAR-1995 US 08/409305,07-JUN-1995 US 08/483554 PR 07-JUN-1995 US 08/487002 PI MARK H SKOLNICK,DAVID E GOLDBERG,YOSHIO MIKI,JEFF SWENSON, PI ALEXANDER KAMB, PI KEITH D HARSHMAN,DONNA M SHATTUCK EIDENS,SEAN V TAVTIGIAN, PI ROGER W WISEMAN, PI ANDREW P FUTREAL PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/68,C12N15/00,C12N5/00 CC Strandedness: Single; CC Topology: Linear; CC Genes sensitive to 17q-chained breast cancer and ovarian CC cancer				
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LOCUS	I77021	30 bp DNA linear	PAT 03-APR-1998		
DEFINITION	Sequence 81 from patent US 5693473.				
ACCESSION	I77021				
VERSION	I77021.1	GI:3013175			
KEYWORDS					

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Job time : 2094.41 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:11:03 ; Search time 196.842 Seconds
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807.979 Million cell updates/sec

Title: US-10-604-726A-6033

Perfect score: 85

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Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PTUS COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	16	18.8	25	3	US-09-396-196G-2452 Sequence 2452, Ap
C 4	16	18.8	25	3	US-09-396-196G-119516 Sequence 119516,
C 5	16	18.8	25	3	US-09-396-196G-119517 Sequence 119517,
C 6	15.6	18.4	25	3	US-09-396-196G-119518 Sequence 119518,
C 7	15.4	18.1	25	3	US-09-396-196G-10620 Sequence 10620, A
C 8	15.4	18.1	25	3	US-09-396-196G-10621 Sequence 10621, A
C 9	15.4	18.1	25	3	US-09-396-196G-20972 Sequence 20972, A
C 10	15.4	18.1	25	3	US-09-396-196G-50927 Sequence 50927, A
C 11	15.4	18.1	28	4	US-09-795-006A-28 Sequence 28, Appl
C 12	15.4	18.1	30	2	US-08-480-784-81 Sequence 81, Appl
C 13	15.4	18.1	30	2	US-08-483-553-81 Sequence 81, Appl
C 14	15.4	18.1	30	2	US-08-487-002-81 Sequence 81, Appl
C 15	15.4	18.1	30	2	US-08-483-554B-81 Sequence 81, Appl
C 16	15.4	18.1	30	2	US-08-488-011B-81 Sequence 81, Appl
C 17	15.4	18.1	30	3	US-08-850-727-81 Sequence 81, Appl
C 18	15.4	18.1	30	7	PCT-US95-10202-81 Sequence 81, Appl
C 19	15.4	18.1	30	7	PCT-US95-10203-81 Sequence 81, Appl
C 20	15.4	18.1	30	7	PCT-US95-10203-81 Sequence 81, Appl
C 21	15.2	17.9	28	3	US-08-814-052-53 Sequence 53, Appl
C 22	15	17.6	24	2	US-09-002-177-5 Sequence 5, Appl
C 23	15	17.6	24	3	US-09-374-584-5 Sequence 5, Appl

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C 26	15	17.6	25	3	US-09-396-196G-12191	Sequence 12191, A
C 27	15	17.6	25	3	US-09-396-196G-43541	Sequence 43541, A
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C 29	15	17.6	26	2	US-08-229-781-48	Sequence 48, Appl
C 30	15	17.6	26	2	US-08-630-918-48	Sequence 48, Appl
C 31	15	17.6	26	3	US-09-004-423-48	Sequence 48, Appl
C 32	15	17.6	26	3	US-09-918-568-48	Sequence 48, Appl
C 33	14.8	17.4	22	2	US-08-244-123-4	Sequence 4, Appl
C 34	14.8	17.4	22	2	US-08-244-122-6	Sequence 6, Appl
C 35	14.8	17.4	22	3	US-09-117-927-12	Sequence 12, Appl
C 36	14.8	17.4	22	3	US-09-117-927-14	Sequence 14, Appl
C 37	14.8	17.4	22	3	US-09-308-090-3	Sequence 3, Appl
C 38	14.8	17.4	22	3	US-09-380-090A-3	Sequence 3, Appl
C 39	14.8	17.4	27	2	US-08-167-113-10	Sequence 10, Appl
C 40	14.8	17.4	27	2	US-08-886-161-10	Sequence 10, Appl
C 41	14.8	17.4	29	2	US-07-931-473B-45	Sequence 45, Appl
C 42	14.8	17.4	29	2	US-07-714-131C-45	Sequence 45, Appl
C 43	14.8	17.4	29	2	US-08-412-110-45	Sequence 45, Appl
C 44	14.8	17.4	29	2	US-08-409-442A-45	Sequence 45, Appl
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ALIGNMENTS

RESULT 1
US-09-396-196G-15707/c
; Sequence 15707, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15707
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-15707

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; Patent No. 6858210
; GENERAL INFORMATION:
; APPLICANT: Marquis, M. David
; APPLICANT: Iverson, M. Gilbert
; APPLICANT: Victoria, J. Edward
; APPLICANT: Jones, S. David
; APPLICANT: Linnik, Matthew
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC DOMAIN 1
; TITLE OF INVENTION: (2GPI POLYPEPTIDES AND METHODS OF USING SAME
; FILE REFERENCE: 252312006900
; CURRENT APPLICATION NUMBER: US/09/328,199

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; EARLIER APPLICATION NUMBER: 60/088,656
; EARLIER FILING DATE: 1998-06-09
; EARLIER APPLICATION NUMBER: 60/103,088
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 30
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-328-199-18

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; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2452
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; ORGANISM: Mus musculus
US-09-396-196G-2452

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; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119516
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-119516

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Db 2 TCGTGTTCCTGCTGCTACAAAGTCC 25

RESULT 5
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; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119517
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-119517

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RESULT 6
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; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
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; ORGANISM: Mus musculus
US-09-396-196G-119518

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; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10620
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-10620

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; Sequence 10621, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
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; SEQ ID NO 10621
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-10621

Query Match 18.1%; Score 15.4; DB 3; Length 25;
Best Local Similarity 68.0%; Pred. No. 1.8e+04;
Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 31 AGCGUCCCAAGUUGAAGGCGC 55
Db 1 AGGCATCCCAACGTGCTAGCGCG 25

RESULT 9
US-09-396-196G-20972
; Sequence 20972, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20972
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-20972

Query Match 18.1%; Score 15.4; DB 3; Length 25;
Best Local Similarity 60.0%; Pred. No. 1.8e+04;
Matches 15; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 40 CAAUUGAAGGCGCCUUGCUUCU 64
Db 1 CAAAGCTGGAAGGCGCGAGGCTTAT 25

RESULT 10
US-09-396-196G-50927/c
; Sequence 50927, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50927
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-50927

Query Match 18.1%; Score 15.4; DB 3; Length 25;
Best Local Similarity 44.0%; Pred. No. 1.8e+04;
Matches 11; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 60 CUUCUGUUUUCUGAUGCAGAGUCC 84
Db 25 CTTGTGTCATCTGTGTGAAGAGTCC 1

RESULT 11
US-09-795-006A-28
; Sequence 28, Application US/09795006A
; Patent No. 6965010
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
```

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; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial chimeric
; OTHER INFORMATION: oligonucleotide sequence derived from multiple vertebrate vascula
; OTHER INFORMATION: endothelial growth factor
US-09-795-006A-28

Query Match      18.1%; Score 15.4; DB 4; Length 28;
Best Local Similarity 64.0%; Pred.No. 1.9e+04;
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      2  GGUUAUCUGCAACUCGAGAGGGGCGUG 26
      || : ||||| ||||| : ||
Db      3  GGGTTGCTGCAATAGTAGGGGCTG 27

RESULT 12
US-08-480-784-81
; Sequence 81, Application US/08480784
; Patent No. 5693473
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Goldgar, David E.
; APPLICANT: Miki, Yoshio
; APPLICANT: Swenson, Jeff
; APPLICANT: Kamb, Alexander
; APPLICANT: Harehman, Keith D.
; APPLICANT: Shattuck-Eidens, Donna M.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Wiseman, Roger W.
; APPLICANT: Futreal, P. Andrew
; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
; TITLE OF INVENTION: Susceptibility Gene
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,784
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/409,305
; FILING DATE: 24-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,824
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,104
; FILING DATE: 16-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,266
; FILING DATE: 02-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,221
; FILING DATE: 12-AUG-1994

```


/ FILING DATE: 02-SEP-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/289,221
/ FILING DATE: 12-AUG-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ihnen, Jeffrey L.
/ REGISTRATION NUMBER: 28,957
/ REFERENCE/DOCKET NUMBER: 24884-109347
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-962-4810
/ TELEFAX: 202-962-8300
/ INFORMATION FOR SEQ ID NO: 81:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 30 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ US-08-483-553-81

Query Match 18.1%; Score 15.4; DB 2; Length 30;
Best Local Similarity 36.0%; Pred. No. 2e+04;
Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 55 CUUUGCUUCUGUUUCUGGAUGCAG 79
| : ||| : : ||| : : |||
Db 6 CTCGTGTTGTTCTCTGTCCTCCAG 30

RESULT 14
US-08-487-002-81
/ Sequence 81, Application US/08487002
/ Patent No. 5710001
/ GENERAL INFORMATION:
/ APPLICANT: Shattuck-Eidens, Donna M.
/ APPLICANT: Simard, Jacques
/ APPLICANT: Emi, Mitsuru
/ APPLICANT: Nakamura, Yusuke
/ APPLICANT: Durocher, Francine
/ TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
/ TITLE OF INVENTION: Susceptibility Gene
/ NUMBER OF SEQUENCES: 85
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
/ STREET: 1201 New York Avenue, N.W., Suite 1000
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/487,002
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/409,305
/ FILING DATE: 24-MAR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/348,824
/ FILING DATE: 29-NOV-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/308,104
/ FILING DATE: 16-SEP-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/300,266
/ FILING DATE: 02-SEP-1994

/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/289,221
/ FILING DATE: 12-AUG-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ihnen, Jeffrey L.
/ REGISTRATION NUMBER: 28,957
/ REFERENCE/DOCKET NUMBER: 24884-109347
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-962-4810
/ TELEFAX: 202-962-8300
/ INFORMATION FOR SEQ ID NO: 81:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 30 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ US-08-487-002-81

Query Match 18.1%; Score 15.4; DB 2; Length 30;
Best Local Similarity 36.0%; Pred. No. 2e+04;
Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 55 CUUUGCUUCUGUUUCUGGAUGCAG 79
| : ||| : : ||| : : |||
Db 6 CTCGTGTTGTTCTCTGTCCTCCAG 30

RESULT 15
US-08-483-554B-81
/ Sequence 81, Application US/08483554B
/ Patent No. 5747282
/ GENERAL INFORMATION:
/ APPLICANT: Skolnick, Mark H.
/ APPLICANT: Goldgar, David E.
/ APPLICANT: Miki, Yoshio
/ APPLICANT: Swenson, Jeff
/ APPLICANT: Kamb, Alexander
/ APPLICANT: Harshman, Keith D.
/ APPLICANT: Shattuck-Eidens, Donna M.
/ APPLICANT: Tavtigian, Sean V.
/ APPLICANT: Wiseman, Roger W.
/ APPLICANT: Futreal, P. Andrew
/ TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
/ TITLE OF INVENTION: Susceptibility Gene
/ NUMBER OF SEQUENCES: 85
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
/ STREET: 1201 New York Avenue, N.W., Suite 1000
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/483,554B
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/409,305
/ FILING DATE: 24-MAR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/348,824
/ FILING DATE: 29-NOV-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/308,104

; FILING DATE: 16-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,266
; FILING DATE: 02-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,221
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109347
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-483-554B-81

Query Match 18.1%; Score 15.4; DB 2; Length 30;
Best Local Similarity 36.0%; Pred. No. 2e+04;
Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
Qy 55 CUUUGCUUCUGUUUUGUGAUGCAG 79
| : || : | : | : | : ||
Db 6 CTCGTGTGTGTTCTCTGTCTCCAG 30

Search completed: October 16, 2006, 14:47:13
Job time : 197.842 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:04:23 ; Search time 3655.64 Seconds
(without alignments)
1300.222 Million cell updates/sec

Title: US-10-604-726A-6033
Perfect score: 85
Sequence: 1 ggguaucugcaacugagag.....uuuucuggaagcagaguccu 85

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 56556

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_hsc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gsa1:*
12: gb_gsa2:*
13: gb_gsa3:*
14: gb_gsa4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	16.2	19.1	25	13	CZ910028 4018012H1
C 2	16	18.8	30	10	H25855 Y153h05.s1
C 3	15.4	18.1	22	11	AZ814281 2M0082L04
4	15.4	18.1	28	11	AZ583022 1M0376A16
C 5	14.6	17.2	25	9	D19580 MUSGS00987
6	14.4	16.9	29	11	BZ292979 SALK_1290
7	14.2	16.7	20	11	AZ469472 1M0283A06
8	14.2	16.7	23	11	AZ785027 2M0028H03
9	14	16.5	24	11	AZ806300 2M0068F13
10	13.4	15.8	26	2	BF732161 EST-NGR-1
C 11	13.4	15.8	27	11	AZ763057 1M0558C22
C 12	13.4	15.8	27	14	AJ591134 Arabidops
C 13	13.4	15.8	29	11	BH792654 SALK_0648
C 14	13.4	15.8	29	11	BH809983 SALK_0368
C 15	13.2	15.5	27	9	DN955347 it86c09.g
16	13.2	15.5	28	1	AA961904 or68c12.s
C 17	13.2	15.5	28	13	CZ482297 604545-5p
18	13.2	15.5	28	14	AJ531105 Arabidops
19	13.2	15.5	29	13	CZ471342 d00034-5p

C 20	13	15.3	28	11	BH851575
C 21	13	15.3	30	11	AZ788334 2M0035B19
C 22	12.8	15.1	21	14	ATH527468 Arabidops
23	12.8	15.1	25	1	AI143800
24	12.8	15.1	27	11	AZ320101 1M0040B04
25	12.8	15.1	27	14	AG203779 Pan trogl
C 26	12.8	15.1	28	13	CZ469769 c05173-3p
C 27	12.8	15.1	28	13	CZ471273 c07136-3p
C 28	12.8	15.1	30	11	AZ375590 1M0129H06
C 29	12.6	14.8	27	11	AZ876196 2M0191A12
30	12.6	14.8	28	11	AZ832180 2M0112J24
C 31	12.6	14.8	28	11	BH790976 SALK_0583
32	12.6	14.8	28	13	CZ481452 603694-5p
33	12.6	14.8	29	11	AZ309550 1M0016A11
34	12.6	14.8	30	13	CZ194878 PST13293-
35	12.6	14.8	30	13	CZ488898 f06234-5p
36	12.4	14.6	22	14	TA219C09P
C 37	12.4	14.6	24	11	BZ356062 SALK_1280
38	12.4	14.6	25	11	AZ945526 2M0206L22
39	12.4	14.6	26	14	AG190196 Pan trogl
40	12.4	14.6	26	14	TA216H03P
41	12.4	14.6	27	5	CF311022
42	12.4	14.6	28	8	CX011229
43	12.4	14.6	28	10	DV227849
44	12.4	14.6	28	10	AZ802448
45	12.4	14.6	28	14	AJ598500 Arabidops

ALIGNMENTS

RESULT 1
CZ910028/c
LOCUS
DEFINITION 4018012H1.1EL.y1 4018 - RescueMu Grid X Zea mays genomic, genomic survey sequence.
ACCESSION CZ910028
VERSION CZ910028.1 GI:71923396
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 25)
AUTHORS Walbot.V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4018012 row: H column: 11
Class: transposon-tagged.
Location/Qualifiers
1..25
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4018 - RescueMu Grid X"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA."

Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

FEATURES
source

Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4018012 row: H column: 11
Class: transposon-tagged.
Location/Qualifiers
1..25
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4018 - RescueMu Grid X"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA."

Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid X was grown at UCSD in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN
Query Match 19.1%; Score 16.2; DB 13; Length 25;
Best Local Similarity 38.1%; Pred. No. 1.3e+06;
Matches 8; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 50 GGGCGCUCUCUCUCUCUCUC 70

Db ||||| :||:::|:::|
23 GGGCTCTTTGTTTGTTC 3

RESULT 2
H25855/C
LOCUS
DEFINITION
Y153h05.s1 Soares breast 3NBH8t Homo sapiens cDNA clone
IMAGE:162009 3' similar to gb:S71043_rnal IG ALPHA-2 CHAIN C REGION
(HUMAN);, mRNA sequence.

ACCESSION H25855

VERSION H25855.1 GI:894978

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE
AUTHORS
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.

1 (bases 1 to 30)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: estewatson.wustl.edu

Insert Size: 934

High quality sequence starts: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 934 Std Error: 0.00

Seq primer: Promega -2lm13

High quality sequence stop: 1.

Location/Qualifiers

1. .30

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GBD:576220"

/db_xref="taxon:9606"

/clone="IMAGE:162009"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares breast 3NBH8t"

/note="Organ: breast; Vector: pT7T3D (Pharmacia) with a

modified Polylinker; site 1: Not I; site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTACCAATCTGAATGGAGCGCCCTTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of a modified pT7T3 vector (Pharmacia).
Library went through one round of normalization to a Cot =
20. Library constructed by Bento Soares and M.Fatima
Bonaldo."

ORIGIN
Query Match 18.8%; Score 16; DB 10; Length 30;
Best Local Similarity 66.7%; Pred. No. 1.5e+06;
Matches 16; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 37 CCCCAAGUUGGAGGCGCUUUGC 60

Db ||||| :||:::|:::|
29 CCTCAAGTGGGAGAGCGCTGTC 6

RESULT 3

AZ814281

LOCUS

DEFINITION

2M0082L04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0082L04 F, genomic survey sequence.

ACCESSION AZ814281

VERSION AZ814281.1 GI:12984285

KEYWORDS GSS.

SOURCE Mus musculus

ORGANISM Mus musculus (house mouse)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D. Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0082 Row: 1 Column: 04

Seq primer: CTTTGTAAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0082L04"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 18.1%; Score 15.4; DB 11; Length 22;

Best Local Similarity 47.1%; Pred. No. 2.3e+06;

Matches 8; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 61 UUCUGUUUCUGGAGC 77

Db 4 :||:|||||

2 TTCTGTTTCGAGC 20

RESULT 4

AZ583022

LOCUS 28 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0376A16R Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0376A16 R, genomic survey sequence.

ACCESSION AZ583022

VERSION AZ583022.1 GI:11702488

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 28)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0376 row: A column: 16

Seq primer: CACACAGGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 28.

FEATURES

source

Location/Qualifiers

1..28

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCLM0376A16"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGCLM library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (GI|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 18.1%; Score 15.4; DB 11; Length 28;

Best Local Similarity 44.0%; Pred. No. 2.4e+06;

Matches 11; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 56 UUGUGUUCUGUUUCUGGAGCAGCA 80

Db 2 TTCCCTCCAGGTTTCTGAATGCAGA 26

RESULT 5

D19580/c

LOCUS

DEFINITION MUSGS00987 Mouse 3'-directed Mus musculus cDNA clone mb1686 3', mRNA sequence.

ACCESSION D19580

VERSION D19580.1 GI:1089438

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 25)

Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and Matsubara,K.

Analysis of gene expression in mouse embryogenesis by 3'-directed

cDNA sequencing

Unpublished (1995)

Contact: Shoko Kawamoto

Institute for Cellular and Molecular Biology

Osaka University

1-3, Yamadaoka, Suita, Osaka, 565, Japan

Email: shoko@next.imcb.osaka-u.ac.jp.

FEATURES

source

1..25

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="mb1686"

/tissue_type="decidual tissue (day 6.5-8.5 of gestation)"

/clone_lib="Mouse 3'-directed"

ORIGIN

Query Match

Best Local Similarity 17.2%; Score 14.6; DB 9; Length 25;

Matches 5; Conservative 12; Mismatches 4; Indels 0; Gaps 0;

QY 55 CUUUGCUUCUGUUUCUGGAGU 75

Db 22 CTTTCTTTTCTTTTGTGAT 2

RESULT 6

LOCUS

DEFINITION BZ292979 29 bp DNA linear GSS 24-OCT-2002

SALK 129051.26.25.x Arabidopsis thaliana TDNA insertion lines

Arabidopsis thaliana genomic clone SALK_129051.26.25.x, genomic

survey sequence.

BZ292979

VERSION BZ292979.1 GI:24340856

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

```

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 29)
Alonso,J.M., Leisae,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..29
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/scotopes="Col-0"
/db_xref="taxon:3702"
/clone="SALK 129051.26.25.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"

ORIGIN
Query Match 16.9%; Score 14.4; DB 11; Length 29;
Best Local Similarity 37.5%; Pred. No. 5.2e+06;
Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 58 UGCUUCUGUUUCUGG 73
:|::|::|::|::|
Db 8 TTCTCTGTTTCTGG 23

RESULT 7
AZ469472 20 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0283A06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0283A06 F, genomic survey sequence.
ACCESSION AZ469472
VERSION GI:10627597
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

```

```

Plate: 0283 row: A column: 06
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0283A06"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 16.7%; Score 14.2; DB 11; Length 20;
Best Local Similarity 31.6%; Pred. No. 5.7e+06;
Matches 6; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 53 CGCUUGUCUUCUGUUUCU 71
:|::|::|::|::|
Db 1 CGCTCTGCTTTTGTGTTT 19

RESULT 8
AZ785027 23 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0028H03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0028H03 R, genomic survey sequence.
ACCESSION AZ785027
VERSION GI:12921357
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

```

This EST fragment was amplified from mouse GR-1+ myeloid progenitor cells CDNA Library with GLGI technique (Generation of Longer cDNA

fragments from SAGE tags for Gene Identification, Proc. Natl. Acad. Sci USA 97, 349, 2000), which starts from the 3' end till the last CAG site of the target cDNA sequence.
Seq primer: M13 Forward.

FEATURES

```

source
1. .26
  /organism="Mus musculus"
  /mol_type="mRNA"
  /strain="C57BL/6"
  /db_xref="taxon:10090"
  /sex="female"
  /tissue_type="bone marrow"
  /cell_type="GR-1+ myeloid progenitor cells"
  /clone_lib="mouse GR-1+ myeloid progenitor cells cDNA
  Library"

```

ORIGIN

```

Query Match      15.8%; Score 13.4; DB 2; Length 26;
Best Local Similarity 26.1%; Pred. No. 1.1e+07;
Matches 6; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

```

```

Oy 56 UUGUCUUGUUGUUGUUGCA 78
   :: :: :::: ||:: ||
Db 2 TTTTITTTTTTTTCGGCTGCA 24

```

RESULT 11

```

AZ763057/c
LOCUS
DEFINITION
  AZ763057 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0558C22 F, genomic survey sequence.

```

```

ACCESSION
  AZ763057.1 GI:12873702

```

```

VERSION
  GSS.

```

```

KEYWORDS
  Mus musculus (house mouse)

```

```

SOURCE
  Mus musculus

```

ORGANISM

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.

```

```

1 (bases 1 to 27)

```

```

REFERENCE
  AUTHORS
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D., Weiss,R.

```

```

  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts

```

```

Unpublished (2000)

```

```

Contact: Robert B. Weiss

```

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University of Utah Genome Center

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University of Utah

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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

```

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84112, USA

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Tel: 801 585 5606

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Fax: 801 585 7177

```

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Email: ddunn@genetics.utah.edu

```

```

Insert Length: 10000 Std Error: 0.00

```

```

Plate: 0558 row: C column: 22

```

```

Seq primer: CGTGTAAACGACGGCCAGT

```

```

Class: plasmid ends

```

```

High quality sequence stop: 27.

```

FEATURES

```

source
1. .27
  /organism="Mus musculus"
  /mol_type="genomic DNA"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="UUGC1M0558C22"
  /sex="Male"
  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
  /clone_lib="Mouse 10kb plasmid UUGC1M library"
  /notes="Vector: PWD42nv; Purified genomic DNA from M.
  musculus C57BL/6J (male) was obtained from the Jackson
  Laboratory Mouse DNA Resource

```

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

```

Query Match      15.8%; Score 13.4; DB 11; Length 27;
Best Local Similarity 65.2%; Pred. No. 1.1e+07;
Matches 15; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

```

```

Oy 9 UGCAACUGAGAGGGCGUGGUAA 31
   :||| ||||| ||||| |||
Db 23 TGCCACGGTGCAGGTGCAGGCTAA 1

```

RESULT 12

```

AJ591134/c
LOCUS
DEFINITION
  AJ591134 Arabidopsis thaliana T-DNA flanking sequence, left border, clone
  580805, genomic survey sequence.

```

```

ACCESSION
  AJ591134 GI:37940758

```

```

VERSION
  GSS; left border; T-DNA flanking sequence.

```

```

KEYWORDS
  Arabidopsis thaliana (thale cress)

```

```

SOURCE
  Arabidopsis thaliana

```

ORGANISM

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

```

REFERENCE

```

  Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
  Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
  Lepiniec,L., Caboche,M. and Lecharny,A.

```

```

  T-DNA integration into the Arabidopsis genome depends on sequences
  of pre-insertion sites

```

```

EMBO Rep. 3 (12), 1152-1157 (2002)

```

```

2 (bases 1 to 27)

```

```

Balzergue,S.

```

```

Direct Submission

```

```

Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue

```

```

Gaston Cremieux, 91057 Evry cedex, FRANCE

```

```

PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).

```

```

Location/Qualifiers

```

```

1. .27

```

```

/organism="Arabidopsis thaliana"

```

```

/mol_type="genomic DNA"

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```

/db_xref="taxon:3702"

```

```

/clone="580805"

```

```

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

```

```

/ecotype="Wassilewskija"

```

```

1. .27

```

```

misc_feature

```


Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Seq primer: -21Mi3UnivRev.

FEATURES

source
 1. .27
 Location/Qualifiers
 /organism="Gnetum gnemon"
 /mol_type="mRNA"
 /db_xref="taxon:3382"
 /sex="female"
 /clone_lib="Gnetum female cone (NYBG)"
 /notes="Organ: mature, unfertilized reproductive strobili;
 Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
 Completed 02/11/02, submitted for sequencing 02/12/02.
 Library: Stratagene ZAP Express cDNA Synthesis Kit. The
 library was size-fractionated to enrich for large inserts.
 Sample: NYBG accession number #436/84"

ORIGIN

Query Match 15.5%; Score 13.2; DB 9; Length 27;
 Best Local Similarity 50.0%; Pred. No. 1.3e+07;
 Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 Qy 50 GGGCGCUCUCUCUCUCU 67
 ||||| :||| :| :
 Db 27 GGGCGTTTGTCTGCT 10

Search completed: October 16, 2006, 15:51:26
 Job time : 3658.64 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 13:53:09 ; Search time 444.812 Seconds
(without alignments)
1332.341 Million cell updates/sec

Title: US-10-604-726A-6033

Perfect score: 85

Sequence: 1 ggguaucgacacagagag.....uuuucggaugcagaguccu 85

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 4443654

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_8.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*
- 15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17.2	20.2	26	6 AAD25159	Aad25159 Human NOV
C 2	17.2	20.2	26	11 ADK51090	Adk51090 Human NOV
C 3	16.2	19.1	23	10 ADE03643	Ade03643 BGS PCR p
C 4	16.2	19.1	29	4 AAH74161	Aah74161 Human neu
C 5	16.2	19.1	30	3 AAZ29694	Aaz29694 Oligonucl
6	16.2	19.1	30	14 AED56453	Aed56453 Human ost
7	15.8	18.6	24	6 ABQ11002	Abq11002 Oligonucl
8	15.8	18.6	24	6 ABQ04674	Abq04674 Oligonucl
C 9	15.8	18.6	24	6 ABQ04715	Abq04715 Oligonucl
C 10	15.8	18.6	24	6 ABQ00358	Abq00358 Oligonucl
C 11	15.8	18.6	24	6 ABQ11043	Abq11043 Oligonucl
C 12	15.8	18.6	25	6 ABQ12538	Abq12538 Oligonucl
C 13	15.8	18.6	25	6 ABQ12579	Abq12579 Oligonucl
14	15.6	18.4	30	14 ADY01452	Ady01452 PCR prime
15	15.6	18.4	30	14 ADY03184	Ady03184 PCR prime
16	15.6	18.4	30	14 ADX84276	Adx84276 DNA ampli
17	15.6	18.4	30	14 AED57194	Aed57194 Human ost
18	15.6	18.4	30	14 AED57246	Aed57246 Human ost

c	19	15.6	18.4	30	15	AEF08297	Aef08297 LOC115209
	20	15.4	18.1	25	9	ACI82438	ACI82438 Human mic
	21	15.4	18.1	28	4	AA512826	AA512826 Human VEG
	22	15.4	18.1	30	14	ADX84134	Adx84134 DNA ampli
	23	15.2	17.9	20	12	ADK75812	Adk75812 Chimeric
	24	15.2	17.9	21	12	ADQ61714	Adq61714 Anti-NR1D
	25	15.2	17.9	21	14	ABE01688	Abe01688 G protein
	26	15.2	17.9	21	14	ABE01687	Abk00740 Human mic
c	27	15.2	17.9	25	9	ACK26430	Aat74315 PCR prime
	28	15.2	17.9	28	2	AAT74315	Aat74315 PCR prime
	29	15.2	17.9	29	15	ABE67632	Aee67632 Human Hun
	30	15.2	17.9	30	12	ADO05844	Ado05844 Teneurin-
	31	15.2	17.9	30	12	ADO05844	Ado05844 Teneurin-
	32	15	17.6	17	4	ABK00741	Abk00741 Human PCR prime
c	33	15	17.6	17	4	ABK00742	Abk00742 Human NOG
c	34	15	17.6	17	4	ABK00740	Abk00740 Human NOG
c	35	15	17.6	23	14	AEC92288	Aec92288 Human IRT
c	36	15	17.6	24	2	AAH78730	Aax78730 Dengue vi
c	37	15	17.6	24	2	ABA94895	Abas94895 Dengue vi
	38	15	17.6	24	14	AEA40055	Aea40055 Brassica
	39	15	17.6	25	1	AAH80648	Aan80648 Sequence
	40	15	17.6	25	1	AAH80647	Aan80647 Sequence
c	41	15	17.6	25	9	ACI58550	ACI58550 Human mic
c	42	15	17.6	25	9	ACI59178	ACI59178 Human mic
c	43	15	17.6	26	2	AAQ72851	Aaq72851 Primer 32
c	44	14.8	17.4	20	10	ABZ89358	Abz89358 Human oli
c	45	14.8	17.4	20	11	ABD25588	Abd25588 AI001174-

ALIGNMENTS

RESULT 1

AAD25159/c

ID AAD25159 standard; DNA; 26 BP.

XX AAD25159;

AC AAD25159;

XX 12-MAR-2002 (first entry)

XX Human NOV4 gene expression assessing Ag1252 probe.

XX Human; NOV4; gene therapy; atherosclerosis; cardiomyopathy; leukaemia;
XX neurological; neurodegenerative disease; cell signalling; inflammation;
XX diabetes; seizure; muscular dystrophy; epilepsy; allergy; adenocarcinoma;
XX coagulation disorder; reproductive; respiratory; bone; nephrological;
XX multiple sclerosis; mental depression; gastro-intestinal disease; cancer;
XX urinary system disorder; Addison's disease; migraine; dermatomyositis;
XX bronchitis; probe; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT modified_base 1

FT /*tag= a

FT /mod_base= OTHER

FT /note= "FAM labelled adenosine"

FT modified_base 26

FT /*tag= b

FT /mod_base= OTHER

FT /note= "TAMRA labelled thymidine"

XX WO200194416-A2.

XX 13-DEC-2001.

XX 07-JUN-2001; 2001WO-US018675.

XX 07-JUN-2000; 2000US-0209927P.

XX 07-JUN-2000; 2000US-0209928P.

XX 07-JUN-2000; 2000US-0210091P.

XX 08-JUN-2000; 2000US-0210208P.

XX 08-JUN-2000; 2000US-0210425P.

XX	US2003195163-A1.	Unidentified.	XX
XX	16-OCT-2003.	CN1287171-A.	XX
XX	11-JUL-2002; 2002US-00193477.	14-MAR-2001.	XX
XX	11-JUL-2001; 2001US-0304888P.	07-SEP-1999; 99CN-00118819.	XX
XX	12-APR-2002; 2002US-0372147P.	07-SEP-1999; 99CN-00118819.	XX
XX	(WUSS/) WU S.	(UYFU-) UNIV FUDAN.	XX
XX	(KEYS/) KRYSTEK S R.	Yu L, Fu Q, Zhao Y;	XX
XX	(LEEL/) LEE L.	WPI; 2001-398934/43.	XX
XX	(FEDE/) FEDER J N.	Human neuron calcium sensing protein and its code sequence, preparation and use.	XX
XX	(CHEN/) CHENG J D.	Example 4; Page 13(Disclosure); 21pp; Chinese.	XX
XX	Wu S, Krystek SR, Lee L, Feder JN, Cheng JD;	The present invention provides the cDNA sequence of human neuronal calcium sensor protein 1 (NCS-1). The NCS-1 protein is a member of the neuronal calcium ion binding protein family and a homologue of human NCS-1. The present invention also relates to the protein, the application of the polynucleotide and the polypeptide, and the production process of the polynucleotide and the polypeptide	XX
XX	WPI; 2003-844480/78.	Sequence 29 BP; 6 A; 8 C; 7 G; 8 T; 0 U; 0 Other;	XX
XX	New isolated nucleic acid molecule encoding BGS-2, 3 and 4 polypeptides, useful for preventing, treating or ameliorating a medical condition, e.g. a disorder related to aberrant immunoglobulin cell surface receptor activity.	Query Match 19.1%; Score 16.2; DB 4; Length 29;	XX
XX	Example 4; SEQ ID NO 228; 242pp; English.	Best Local Similarity 58.6%; Pred. No. 4.4e+04;	XX
XX	The invention relates to an isolated nucleic acid molecule encoding BGS-2, 3 and 4 polypeptides. The nucleic acid molecule, polypeptide and methods are useful for preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant immunoglobulin cell surface receptor activity; a cellular adhesion disorder; a disorder related to hyper- or hypo-immunoglobulin receptor activity; a disorder related to aberrant signal transduction; a reproductive disorder; a female reproductive disorder; an ovarian disorder; ovarian cancer, sexual dysfunction; infertility; pelvic inflammatory disease; endometriosis; premature menopause; placental dysfunction; hormone deficiency; oestrogen deficiency; aberrant androgen metabolism; polycystic ovarian disease; aberrant ovarian cycle; dysfunctional uterine bleeding; resistant-ovary syndrome; hermaphroditism; immune disorders; inflammatory disorders; arthritis; asthma; immunodeficiency diseases such as AIDS; leukaemia; inflammatory bowel disease; sepsis; acne; psoriasis; hypersensitivity; such as T-cell mediated cytotoxicity; immune reactions to transplanted organs and tissues; or autoimmunity disorders; autoimmune infertility; Addison's disease; haemolytic anaemia; rheumatoid arthritis; dermatitis; glomerulonephritis; Graves' Disease; Multiple Sclerosis; Myasthenia gravis; Systemic lupus Erythematosus; insulin dependent diabetes mellitus ; autoimmune inflammatory eye disease; Sjogren's disease; and scleroderma. The present sequence is used in the exemplification of the present invention.	Matches 17; Conservative 4; Mismatches 8; Indels 0; Gaps 0;	XX
XX	Sequence 23 BP; 2 A; 4 C; 5 G; 12 T; 0 U; 0 Other;	QY 14 CUGAGAGGGGUGUUAAGGCGUCCCA 42	XX
XX	Query Match 19.1%; Score 16.2; DB 10; Length 23;	DB 29 CTACGACGGCTGGTATAGGAATTCCTCA 1	XX
XX	Best Local Similarity 38.1%; Pred. No. 4.1e+04;	RESULT 5	XX
XX	Matches 8; Conservative 10; Mismatches 3; Indels 0; Gaps 0;	AAZ29694	XX
XX	QY 52 GCGCUUGUCUUGUUUCUG 72	ID AAZ29694 standard; DNA; 30 BP.	XX
XX	DB 1 GCGCTTGTATATGTTCTCTG 21	XX AAZ29694;	XX
XX	RESULT 4	XX AAZ29694;	XX
XX	AAH74161/c	DT 22-MAR-2000 (first entry)	XX
XX	ID AAH74161 standard; DNA; 29 BP.	DE Oligonucleotide B2del242-326 for domain deletion mutant of hbeta-2 GPI.	XX
XX	AC AAH74161;	XX Human beta-2 glycoprotein I; hbeta-2 GPI; beta-2 GPI domain 1;	XX
XX	09-OCT-2001 (first entry)	XX oligonucleotide B2del242-326; suahi domain;	XX
XX	Human neuronal calcium sensor protein 1 related oligonucleotide #6.	XX beta-2 GPI-dependent antiphospholipid antibody; as.	XX
XX	Human neuronal calcium sensor protein 1; NCS-1; primer; ds.	XX Homo sapiens.	XX
XX		OS Synthetic.	XX
XX		XX WO9964595-A1.	XX
XX		XX 16-DEC-1999.	XX
XX		XX 09-JUN-1999; 99WO-US013194.	XX
XX		XX 09-JUN-1998; 98US-0088656P.	XX
XX		XX 05-OCT-1998; 98US-0103088P.	XX
XX		XX 08-JUN-1999; 99US-00328199.	XX
XX		XX (LJOL-) LA JOLLA PHARM CO.	XX
XX		XX Marquis DM, Iverson GM, Victoria EJ, Jones DS, Linnik MD;	XX
XX		XX WPI; 2000-116542/10.	XX

```
PT New isolated domain 1 beta-2 GPI polypeptides, used for inhibiting
PT antiphospholipid antibodies for treating, e.g. thrombosis.
XX
PS Example 1; Page 51; 158pp; English.
XX
CC The present sequence is oligonucleotide B2del242-326 used for generating
CC domain deletion mutant of human beta-2 glycoprotein I. Isolated domain I
CC of beta-2 GPI binds to and inhibits beta-2 GPI-dependent antiphospholipid
CC antibodies. Amino acids 242-326 are deleted from beta-2 GPI and the
CC resulting protein contains 1, 2, 3 and 4 sushi domains. This is used to
CC determine the antigenic regions of beta-2 GPI
XX
XX Sequence 30 BP; 6 A; 6 C; 11 G; 7 T; 0 U; 0 Other;
Query Match 19.1%; Score 16.2; DB 3; Length 30;
Best Local Similarity 58.6%; Pred. No. 4.5e+04;
Matches 17; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
XX
QY 25 UGUUUAAGGCGUCCCAAGUGGAGGGC 53
Db 2 TGGTGATGGTGCCCAACTTGCATGGC 30
RESULT 6
AED56453
ID AED56453 standard; DNA; 30 BP.
XX
AC AED56453;
XX
DT 29-DEC-2005 (first entry)
XX
DE Human osteoporosis related SNP primer #413.
XX
KW osteoarthritis; musculoskeletal disease; Antiarthritic; Osteopathic;
KW RNAi; RNAi interference; ADAMTS2 agonist; ss; PCR; primer.
XX
XX Homo sapiens.
XX
PN WO2005100604-A2.
XX
PD 27-OCT-2005.
XX
PF 31-MAR-2005; 2005WO-US010912.
XX
PR 01-APR-2004; 2004US-0559011P.
PR 01-APR-2004; 2004US-0559040P.
PR 01-APR-2004; 2004US-0559042P.
PR 01-APR-2004; 2004US-0559202P.
PR 01-APR-2004; 2004US-0559203P.
PR 01-APR-2004; 2004US-0559225P.
PR 01-APR-2004; 2004US-0559275P.
XX
PA (SEQU-) SEQUENOM INC.
XX
PI Mah S, Braun A, Kammerer SM, Nelson MR, Reneland RH, Langdown ML;
XX
XX WPI; 2005-758634/77.
XX
PT Identifying a subject at risk of osteoarthritis comprises detecting the
PT presence or absence of one or more specified polymorphic variations
PT associated with osteoarthritis in a nucleic acid sample from a subject.
XX
PS Example 5; Page 88; 539pp; English.
XX
CC The invention relates to a method of identifying a subject at risk of
CC osteoarthritis which comprises detecting the presence or absence of one
CC or more polymorphic variations associated with osteoarthritis in a
CC nucleic acid sample where the presence of the polymorphism indicates a
CC risk of osteoarthritis. The method is useful for identifying a subject at
CC risk of osteoarthritis. The method is also useful for identifying agents
CC for treating osteoarthritis. The present sequence represents a PCR primer
CC used to identify single nucleotide polymorphisms associated with
CC osteoporosis.
XX
XX Sequence 30 BP; 4 A; 3 C; 12 G; 11 T; 0 U; 0 Other;
Query Match 19.1%; Score 16.2; DB 14; Length 30;
Best Local Similarity 41.4%; Pred. No. 4.5e+04;
Matches 12; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
XX
QY 41 AAGUUGGAAGGCGCUUUGCUUCUGUUU 69
Db 1 ACGTTGGATGAGTGCCTTTCAGGTGTGT 29
RESULT 7
ABQ11002
ID ABQ11002 standard; DNA; 24 BP.
XX
AC ABQ11002;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 10993.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
PN WO200216649-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026519.
XX
PR 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX
XX (ILLU-) ILLUMINA INC.
XX
XX Gunderson K;
XX
XX WPI; 2002-292068/33.
XX
PT Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
PS Claim 1; Page 225; 261pp; English.
XX
CC The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
XX Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;
Query Match 18.6%; Score 15.8; DB 6; Length 24;
Best Local Similarity 73.7%; Pred. No. 5.9e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
QY 16 GAGAGCGCGUGUUAAGGC 34
Db 4 GAGAGCGCTTGGTTAAGGC 22
RESULT 8
ABQ04674
ID ABQ04674 standard; DNA; 24 BP.
XX
XX ABQ04674;
AC ABQ04674;
```

XX	11-JUN-2002	(first entry)
DT		
XX	Oligonucleotide adapter/capture probe 4665.	
DE		
XX	Oligonucleotide array; adapter sequence; probe; ss.	
KW		
XX	Synthetic.	
OS		
XX	WO200216649-A2.	
PN		
XX	28-FEB-2002.	
PD		
XX		
PF	27-AUG-2001; 2001WO-US026519.	
XX		
XX	25-AUG-2000; 2000US-0227948P.	
PR		
XX	29-AUG-2000; 2000US-0228854P.	
XX		
PA	(ILLU-) ILLUMINA INC.	
XX		
PI	Gunderson K;	
XX		
PI	WPI; 2002-292068/33.	
DR		
XX		
PT	Array comprising adapter sequences useful for immobilizing or detecting a	
PT	target nucleic acid sequence, has different addresses comprising	
PT	different specific capture probes.	
XX		
XX	Claim 1; Page 147; 261pp; English.	
PS		
XX		
CC	The invention relates to an oligonucleotide array (I) comprising at least	
CC	25 different addresses (adapter sequences) with each comprising a	
CC	different capture probe selected from a group consisting of the sequences	
CC	given in ABQ00010-ABQ13409. (I) is useful for immobilising a target	
CC	nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-	
CC	ABQ13409) to a target nucleic acid to form a modified target nucleic acid	
CC	and contacting the modified target nucleic acid with (I). The steps of	
CC	above method is useful for detecting a target nucleic acid, which further	
CC	comprises detecting the presence of the modified target nucleic acid	
XX		
SQ	Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;	
	Query Match 18.6%; Score 15.8; DB 6; Length 24;	
	Best Local Similarity 73.7%; Pred. No. 5.9e+04;	
	Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;	
Qy	16 GAGAGGGCGCUGGUAGGC 34	
	: :	
	4 GAGAGGGCGTTGGTTAAGGC 22	
Db		
	AC ABQ04715;	
XX		
DT	11-JUN-2002 (first entry)	
XX		
XX	Oligonucleotide adapter/capture probe 4706.	
DE		
XX	Oligonucleotide array; adapter sequence; probe; ss.	
KW		
XX	Synthetic.	
OS		
XX	WO200216649-A2.	
PN		
XX	28-FEB-2002.	
PD		
XX		
PF	27-AUG-2001; 2001WO-US026519.	
XX		
XX	25-AUG-2000; 2000US-0227948P.	
PR		
XX	29-AUG-2000; 2000US-0228854P.	
PR		

XX (ILLU-) ILLUMINA INC.
FA Gunderson K;
XX WPI; 2002-292068/33.
XX
XX Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
XX Claim 1; Page 147; 26lpp; English.
PS
XX The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
XX Sequence 24 BP; 5 A; 10 C; 2 G; 7 T; 0 U; 0 Other;
SQ

Query Match 18.6%; Score 15.8; DB 6; Length 24;
Best Local Similarity 73.7%; Pred. No. 5.9e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 16 GAGAGGGCGUGGUAAAGGC 34
||||| |:::|||||
Db 21 GAGAGGGCGTTGGTTAAGGC 3

RESULT 10
ABQ00358
ID ABQ00358 standard; DNA, 24 BP.
XX AC ABQ00358;
XX AC
XX 11-JUN-2002 (first entry)
XX
XX Oligonucleotide adapter/capture probe 349.
XX
XX Oligonucleotide array; adapter sequence; probe; ss.
OS Synthetic.
XX WO200216649-A2.
XX
XX 28-FEB-2002.
XX
XX 27-AUG-2001; 2001WO-US026519.
XX
XX 25-AUG-2000; 2000US-0227948P.
PR
PR 29-AUG-2000; 2000US-0228854P.
XX
XX (ILLU-) ILLUMINA INC.
XX
XX Gunderson K;
FI
XX WPI; 2002-292068/33.
DR
XX Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
XX Claim 1; Page 52; 26lpp; English.
PS
XX The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
XX Sequence 24 BP; 5 A; 10 C; 2 G; 7 T; 0 U; 0 Other;
SQ

CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (1). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 18.6%; Score 15.8; DB 6; Length 24;
Best Local Similarity 73.7%; Pred. No. 5.9e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 16 GAGAGGGCGUGGUUAGGC 34
||||| | : : : : :
DB 4 GAGAGCGTGTGTTAAGC 22

RESULT 11
ABQ11043/c
ID ABQ11043 standard; DNA; 24 BP.
XX
AC ABQ11043;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 11034.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
PN WO200216649-A2.
XX
PD 28-FEB-2002.

XX
PF 27-AUG-2001; 2001WO-US026519.
XX
PR 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX
PA (ILLU-) ILLUMINA INC.
XX
PI Gunderson K;
XX
DR WPI; 2002-292068/33.
XX
PT Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
PS Claim 1; Page 225; 261pp; English.

XX
CC The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 5 A; 10 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 18.6%; Score 15.8; DB 6; Length 24;
Best Local Similarity 73.7%; Pred. No. 5.9e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 16 GAGAGGGCGUGGUUAGGC 34
||||| | : : : : :
DB 21 GAGAGCGTGTGTTAAGC 3

RESULT 12
ABQ12538
ID ABQ12538 standard; DNA; 25 BP.
XX
AC ABQ12538;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 12529.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
PN WO200216649-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026519.
XX
PR 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX
PA (ILLU-) ILLUMINA INC.
XX
PI Gunderson K;
XX
DR WPI; 2002-292068/33.
XX
PT Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
PS Claim 1; Page 244; 261pp; English.

XX
CC The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 25 BP; 7 A; 2 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 18.6%; Score 15.8; DB 6; Length 25;
Best Local Similarity 73.7%; Pred. No. 6e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 16 GAGAGGGCGUGGUUAGGC 34
||||| | : : : : :
DB 5 GAGAGCGTGTGTTAAGC 23

RESULT 13
ABQ12579/c
ID ABQ12579 standard; DNA; 25 BP.
XX
AC ABQ12579;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 12570.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
PN WO200216649-A2.
XX
PD 28-FEB-2002.

XX 27-AUG-2001; 2001WO-US026519.
XX
XX 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX
XX (ILLU-) ILLUMINA INC.
PA
XX Gunderson K;
XX
XX WPI; 2002-292068/33.
XX
XX Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
XX Claim 1; Page 244; 261pp; English.
XX
XX The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
XX Sequence 25 BP; 5 A; 10 C; 2 G; 8 T; 0 U; 0 Other;
SQ

Query Match 18.6%; Score 15.8; DB 6; Length 25;
Best Local Similarity 73.7%; Pred. No. 6e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX

QY 16 GAGAGGGCGGUGUAGGC 34
DB ||||| :||:||||
22 GAGAGCGTGGTAAAGC 4

RESULT 14
ADY01452
ID ADY01452 standard; DNA; 30 BP.
XX
XX ADY01452;
AC
XX
XX 05-MAY-2005 (first entry)
DT
XX
XX PCR primer 156 used to amplify human DPF3 SNP DNA.
DE
XX
XX SNP detection; breast tumor; endocrine disease;
KW gynecology and obstetrics; neoplasm; cytostatic; metastasis;
KW gene therapy; RNA interference; ss; PCR; primer;
KW D4, zinc and double PHD fingers, family 3; DPF3;
KW guanine-nucleotide exchange factor.
XX
XX Homo sapiens.
OS
XX
XX WO2005014846-A2.
PN
XX
XX 17-FEB-2005.
PD
XX
XX 27-MAY-2004; 2004WO-US016939.
PF
XX
XX 24-JUL-2003; 2003US-0490234P.
PR 25-NOV-2003; 2003US-00723681.
PR 25-NOV-2003; 2003US-0525239P.
XX
XX (SEQU-) SEQUENOM INC.
PA
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
PI Hoyal-Wrightson CR;
PI
XX
XX WPI; 2005-163257/17.
DR

XX Identifying risk of, preventing and/or treating breast cancer by
PT identifying and/or analyzing polymorphic variations in nucleotide
PT sequences within the human genome.
XX
XX Example 16; Page 239; 617pp; English.
XX
XX The invention relates to a novel method for identifying a subject at risk
CC of breast cancer comprising detecting the presence or absence of a
CC polymorphic variation associated with breast cancer. The method of the
CC invention demonstrates cytostatic activity and may be useful for
CC identifying a risk of, preventing and/or treating breast cancer and
CC cancer metastasis. The methods may be utilized for gene therapy or RNA
CC interference. The current sequence is that of a PCR primer of the
CC invention which was used to amplify a human rho-family guanine-nucleotide
CC exchange factor D4, zinc and double PHD fingers, family 3 (DPF3) DNA
CC containing a single nucleotide polymorphism (SNP).
XX
XX Sequence 30 BP; 5 A; 7 C; 7 G; 11 T; 0 U; 0 Other;
SQ

Query Match 18.4%; Score 15.6; DB 14; Length 30;
Best Local Similarity 40.0%; Pred. No. 7.6e+04;
Matches 12; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
XX

QY 41 AAGUUGGAAGCGGCUUCUGUUUC 70
DB ||||| :||:||||
1 ACGTTGGATGGGTACATCTTCTGCTTC 30

RESULT 15
ADY03184
ID ADY03184 standard; DNA; 30 BP.
XX
XX ADY03184;
AC
XX
XX 05-MAY-2005 (first entry)
DT
XX
XX PCR primer 7 used to amplify human LOC145197 SNP DNA.
DE
XX
XX SNP detection; breast tumor; endocrine disease;
KW gynecology and obstetrics; neoplasm; cytostatic; metastasis;
KW gene therapy; RNA interference; ds; SNP; single nucleotide polymorphism;
KW LOC145197.
XX
XX Homo sapiens.
OS
XX
XX WO2005014846-A2.
PN
XX
XX 17-FEB-2005.
PD
XX
XX 27-MAY-2004; 2004WO-US016939.
PF
XX
XX 24-JUL-2003; 2003US-0490234P.
PR 25-NOV-2003; 2003US-00723681.
PR 25-NOV-2003; 2003US-0525239P.
XX
XX (SEQU-) SEQUENOM INC.
PA
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
PI Hoyal-Wrightson CR;
PI
XX
XX WPI; 2005-163257/17.
DR

XX Identifying risk of, preventing and/or treating breast cancer by
PT identifying and/or analyzing polymorphic variations in nucleotide
PT sequences within the human genome.
XX
XX Example 17; Page 296; 617pp; English.
XX
XX The invention relates to a novel method for identifying a subject at risk
CC of breast cancer comprising detecting the presence or absence of a
CC polymorphic variation associated with breast cancer. The method of the
CC invention demonstrates cytostatic activity and may be useful for

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:16:09 ; Search time 1197.03 Seconds
(without alignments)
872.534 Million cell updates/sec

Title: US-10-604-726A-6033

Perfect score: 85

Sequence: 1 ggguaucugcaacagagag.....uuuucuggaugcagaguccu 85

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 18922170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 23237482

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18.2	21.4	25	9	US-10-719-900-385230
2	18.2	21.4	25	9	US-10-719-900-453865
3	18.2	21.4	25	11	US-10-933-982-172709
4	18.2	21.4	26	8	US-10-403-161-111
5	18.2	21.4	27	11	US-10-310-914A-166755
6	17.8	20.9	24	10	US-10-750-185-13212
7	17.8	20.9	24	10	US-10-750-623-13212
8	17.6	20.7	24	11	US-10-310-914A-106490
9	17.6	20.7	25	13	US-11-036-317-713202
10	17.6	20.7	25	15	US-11-121-849-282693
11	17.6	20.7	25	15	US-11-121-849-386034
12	17.6	20.7	25	15	US-11-121-849-386035
13	17.6	20.7	25	15	US-11-121-849-386965
14	17.6	20.7	25	15	US-11-121-849-386966
15	17.2	20.2	24	11	US-10-310-914A-776242
16	17.2	20.2	25	3	US-10-719-900-888593
17	17.2	20.2	26	3	US-09-877-843-70

18	17	20.0	25	8	US-10-719-956-28545	Sequence 28545, A
19	17	20.0	25	8	US-10-719-956-411709	Sequence 411709, A
20	17	20.0	25	9	US-10-719-900-593945	Sequence 593945, A
21	17	20.0	25	10	US-10-809-189-15707	Sequence 15707, A
22	17	20.0	25	13	US-11-036-317-648052	Sequence 648052, A
23	17	20.0	25	13	US-11-036-317-705480	Sequence 705480, A
24	17	20.0	25	13	US-11-036-317-908282	Sequence 908282, A
25	17	20.0	25	13	US-11-036-317-989609	Sequence 989609, A
26	17	20.0	25	15	US-11-121-849-271873	Sequence 271873, A
27	17	20.0	25	15	US-11-121-849-568626	Sequence 568626, A
28	17	20.0	25	16	US-11-136-527-348977	Sequence 348977, A
29	16.8	19.8	25	9	US-10-719-900-614920	Sequence 614920, A
30	16.8	19.8	25	11	US-10-310-914A-1047378	Sequence 1047378, A
31	16.8	19.8	25	13	US-11-036-317-640087	Sequence 640087, A
32	16.8	19.8	25	15	US-11-121-849-578380	Sequence 578380, A
33	16.6	19.5	25	8	US-10-719-956-317240	Sequence 317240, A
34	16.6	19.5	25	9	US-10-719-900-385229	Sequence 385229, A
35	16.6	19.5	25	9	US-10-719-900-453864	Sequence 453864, A
36	16.6	19.5	25	9	US-10-719-900-509279	Sequence 509279, A
37	16.6	19.5	25	9	US-10-719-900-559931	Sequence 559931, A
38	16.6	19.5	25	10	US-10-956-157-225474	Sequence 225474, A
39	16.6	19.5	25	11	US-10-310-914A-324009	Sequence 324009, A
40	16.6	19.5	25	11	US-10-310-914A-497082	Sequence 497082, A
41	16.6	19.5	25	11	US-10-932-182A-96809	Sequence 96809, A
42	16.6	19.5	25	11	US-10-933-982-172712	Sequence 172712, A
43	16.6	19.5	25	11	US-10-933-982-172720	Sequence 172720, A
44	16.6	19.5	25	11	US-10-934-048A-56788	Sequence 56788, A
45	16.6	19.5	25	13	US-11-036-317-310318	Sequence 310318, A

ALIGNMENTS

RESULT 1

US-10-719-900-385230
; Sequence 385230, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 385230
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-385230

Query Match 21.4%; Score 18.2; DB 9; Length 25;
Best Local Similarity 43.5%; Pred. No. 1.4e+04;
Matches 10; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 58 UGCUUCUGUUUCUGGAUGCAGA 80

Db 2 TCGTCTGTTTCTGAGTGATA 24

RESULT 2

US-10-719-900-453865
; Sequence 453865, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808


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; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Reverse Primer
US-10-750-185-13212

Query Match
Best Local Similarity 20.9%; Score 17.8; DB 10; Length 24;
Matches 8; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

QY 56 UUUGCUUCUGUUUCUGGAUG 76
Db 1 TTACATCTGTTTCTGGATG 21

RESULT 7
US-10-750-623-13212
; Sequence 13212, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13212
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Reverse Primer
US-10-750-623-13212

Query Match
Best Local Similarity 20.9%; Score 17.8; DB 10; Length 24;
Matches 8; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

QY 56 UUUGCUUCUGUUUCUGGAUG 76
Db 1 TTACATCTGTTTCTGGATG 21

RESULT 8
US-10-310-914A-106490/c
; Sequence 106490, Application US/10310914A
; Publication No. US2006000332A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 106490
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-106490

Query Match
Best Local Similarity 20.7%; Score 17.6; DB 11; Length 24;
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; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Reverse Primer
US-10-750-185-13212

Query Match
Best Local Similarity 20.9%; Score 17.8; DB 10; Length 24;
Matches 8; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

QY 56 UUUGCUUCUGUUUCUGGAUG 76
Db 1 TTACATCTGTTTCTGGATG 21

RESULT 7
US-10-750-623-13212
; Sequence 13212, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13212
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Reverse Primer
US-10-750-623-13212

Query Match
Best Local Similarity 20.9%; Score 17.8; DB 10; Length 24;
Matches 8; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

QY 56 UUUGCUUCUGUUUCUGGAUG 76
Db 1 TTACATCTGTTTCTGGATG 21

RESULT 8
US-10-310-914A-106490/c
; Sequence 106490, Application US/10310914A
; Publication No. US2006000332A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 106490
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-106490

Query Match
Best Local Similarity 20.7%; Score 17.6; DB 11; Length 24;
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Best Local Similarity 45.8%; Pred. No. 2.3e+04;
Matches 11; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 50 GGGCGCUUGCUUGCUUGUUUCUGG 73
Db 24 GGGCACTTGTGCTTCTTCTGG 1

RESULT 9
US-11-036-317-713202/c
; Sequence 713202, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 713202
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-713202

Query Match
Best Local Similarity 20.7%; Score 17.6; DB 13; Length 25;
Matches 16; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 16 GAGAGGGCGUGGUUAGGCGUCCC 39
Db 24 GAGAGGCCCTGGTTCAGGAGTCCC 1

RESULT 10
US-11-121-849-292693
; Sequence 292693, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 292693
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-292693

Query Match
Best Local Similarity 20.7%; Score 17.6; DB 15; Length 25;
Matches 10; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 55 CUUUGCUUCUGUUUCUGGAUGCA 78
Db 1 CTATGCTTAGATTTCGTGATGCA 24

RESULT 11
US-11-121-849-386034/c
; Sequence 386034, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
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/ ; GENERAL INFORMATION:
/ ; APPLICANT: SUNTORY LIMITED
/ ; APPLICANT: NAKAO, YOSHIHIRO
/ ; APPLICANT: NAKAMURA, NORIHISA
/ ; APPLICANT: KODAMA, YUKIKO
/ ; APPLICANT: FUJIMURA, TOMOKO
/ ; APPLICANT: ASHIKARI, TOSHIHIKO
/ ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ ; FILE REFERENCE: S-38-285
/ ; CURRENT APPLICATION NUMBER: US/11/217,529
/ ; CURRENT FILING DATE: 2005-09-02
/ ; PRIOR APPLICATION NUMBER: US 10/932,182
/ ; PRIOR FILING DATE: 2004-09-02
/ ; NUMBER OF SEQ ID NOS: 197023
/ ; SOFTWARE: PatentIn version 3.3
/ ; SEQ ID NO 96809
/ ; LENGTH: 25
/ ; TYPE: DNA
/ ; ORGANISM: Saccharomyces pastorianus
US-11-217-529-96809

Query Match      19.5%; Score 16.6; DB 8; Length 25;
Best Local Similarity 60.9%; Pred. No. 8.9e+03;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 36 UCCCCAAGUUGGAGGCGCUU 58
DB 24 TTCCCAATTGTGAAGGGCGCTT 2

RESULT 3
US-11-217-529-183005
/ ; Sequence 183005, Application US/11217529
/ ; Publication No. US20060099612A1
/ ; GENERAL INFORMATION:
/ ; APPLICANT: SUNTORY LIMITED
/ ; APPLICANT: NAKAO, YOSHIHIRO
/ ; APPLICANT: NAKAMURA, NORIHISA
/ ; APPLICANT: KODAMA, YUKIKO
/ ; APPLICANT: FUJIMURA, TOMOKO
/ ; APPLICANT: ASHIKARI, TOSHIHIKO
/ ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ ; FILE REFERENCE: S-38-285
/ ; CURRENT APPLICATION NUMBER: US/11/217,529
/ ; CURRENT FILING DATE: 2005-09-02
/ ; PRIOR APPLICATION NUMBER: US 10/932,182
/ ; PRIOR FILING DATE: 2004-09-02
/ ; NUMBER OF SEQ ID NOS: 197023
/ ; SOFTWARE: PatentIn version 3.3
/ ; SEQ ID NO 183005
/ ; LENGTH: 25
/ ; TYPE: DNA
/ ; ORGANISM: Saccharomyces pastorianus
US-11-217-529-183005

Query Match      19.3%; Score 16.4; DB 8; Length 25;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 9; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 62 UCUGUUUUCUGGAUGCAG 79
DB 7 TCTGTTTCTGATGCAG 24

RESULT 4
US-11-348-413-960036/c
/ ; Sequence 960036, Application US/11348413
/ ; Publication No. US2006016012A1
/ ; GENERAL INFORMATION:
/ ; APPLICANT: Wyeth
/ ; APPLICANT: Mounts, William M
/ ; APPLICANT: Murphy, Ellen
/ ; APPLICANT: Olmsted, Stephen
```

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/ ; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
/ ; FILE REFERENCE: 031896-084100 (AM 101724)
/ ; CURRENT APPLICATION NUMBER: US/11/348,413
/ ; CURRENT FILING DATE: 2006-02-07
/ ; PRIOR APPLICATION NUMBER: PCT/US05/035471
/ ; PRIOR FILING DATE: 2005-10-05
/ ; PRIOR APPLICATION NUMBER: US 11/243,445
/ ; PRIOR FILING DATE: 2005-10-05
/ ; PRIOR APPLICATION NUMBER: US 60/615,573
/ ; PRIOR FILING DATE: 2004-10-05
/ ; NUMBER OF SEQ ID NOS: 1276209
/ ; SEQ ID NO 960036
/ ; LENGTH: 25
/ ; TYPE: DNA
/ ; ORGANISM: Artificial
/ ; FEATURE:
/ ; OTHER INFORMATION: probe
/ ; FEATURE:
/ ; NAME/KEY: misc feature
/ ; LOCATION: (1)-(25)
/ ; OTHER INFORMATION: SEQ ID NO: 10014; WAN01PG3J_at; Start 207; Stop 231;
/ ; OTHER INFORMATION: 000000000100000
US-11-348-413-960036

Query Match      19.1%; Score 16.2; DB 9; Length 25;
Best Local Similarity 33.3%; Pred. No. 1.3e+04;
Matches 7; Conservative 11; Mismatches 3; Indels 0; Gaps 0;

QY 55 CUUUGCUUCUGUUUCUGGAU 75
DB 23 CTTGGCTTCTGTTTCTACAT 3

RESULT 5
US-11-217-529-52650/c
/ ; Sequence 52650, Application US/11217529
/ ; Publication No. US20060099612A1
/ ; GENERAL INFORMATION:
/ ; APPLICANT: SUNTORY LIMITED
/ ; APPLICANT: NAKAO, YOSHIHIRO
/ ; APPLICANT: NAKAMURA, NORIHISA
/ ; APPLICANT: KODAMA, YUKIKO
/ ; APPLICANT: FUJIMURA, TOMOKO
/ ; APPLICANT: ASHIKARI, TOSHIHIKO
/ ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ ; FILE REFERENCE: S-38-285
/ ; CURRENT APPLICATION NUMBER: US/11/217,529
/ ; CURRENT FILING DATE: 2005-09-02
/ ; PRIOR APPLICATION NUMBER: US 10/932,182
/ ; PRIOR FILING DATE: 2004-09-02
/ ; NUMBER OF SEQ ID NOS: 197023
/ ; SOFTWARE: PatentIn version 3.3
/ ; SEQ ID NO 52650
/ ; LENGTH: 25
/ ; TYPE: DNA
/ ; ORGANISM: Saccharomyces pastorianus
US-11-217-529-52650

Query Match      18.8%; Score 16; DB 8; Length 25;
Best Local Similarity 62.5%; Pred. No. 1.5e+04;
Matches 15; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 34 CGUCCCCAAGUUGAAGGCGCUU 57
DB 24 CGTCCACGACCTGGAAGGGCTCTT 1

RESULT 6
US-11-217-529-98397
/ ; Sequence 98397, Application US/11217529
/ ; Publication No. US20060099612A1
/ ; GENERAL INFORMATION:
/ ; APPLICANT: SUNTORY LIMITED
```

```
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 98397
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-98397

Query Match      18.6%; Score 15.8; DB 8; Length 25;
Best Local Similarity 36.8%; Pred. No. 1.1e+04;
Matches 7; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 54 GCUUGCUUCUGUUUCUG 72
DB 4 GCTTTCCTCTGCTTATG 22

RESULT 7
US-11-217-529-29948/c
; Sequence 29948, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29948
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-29948

Query Match      18.4%; Score 15.6; DB 8; Length 25;
Best Local Similarity 45.5%; Pred. No. 2.1e+04;
Matches 10; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 64 UGUUUUCUGAUGCAGAGUCCU 85
DB 24 TGTTTGGAGATGCACGCTCT 3

RESULT 8
US-11-217-529-94477/c
; Sequence 94477, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
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```
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94477
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-94477

Query Match      18.4%; Score 15.6; DB 8; Length 25;
Best Local Similarity 50.0%; Pred. No. 2.1e+04;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 47 GAAGGGCGCUUCUGUUGUUU 68
DB 24 GGAGGGCGCTGACTTCTGTCT 3

RESULT 9
US-11-217-529-99137
; Sequence 99137, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 99137
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-99137

Query Match      18.4%; Score 15.6; DB 8; Length 25;
Best Local Similarity 36.4%; Pred. No. 2.1e+04;
Matches 8; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 55 CUUUGCUUCUGUUUCUGAUG 76
DB 2 CTATGCTTCTATGTTCTGTG 23

RESULT 10
US-11-348-413-411718/c
; Sequence 411718, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
```

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; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 411718
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 12488; WAN01UOM6; Start 38; Stop 62;
; OTHER INFORMATION: 00000000011110
US-11-348-413-411718
```

```
Query Match      18.4%; Score 15.6; DB 9; Length 25;
Best Local Similarity 36.4%; Pred. No. 2.1e+04;
Matches 8; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
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```
QY 54 GCUUUGUCUCUGUUUCUGGAU 75
Db 25 GGTGTGTTCTGTATCTGGAT 4
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RESULT 11

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US-11-348-413-414079/c
; Sequence 414079, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 414079
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 12552; WAN01UOO2; Start 494; Stop 518;
; OTHER INFORMATION: 00000000011111
US-11-348-413-414079
```

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Query Match      18.4%; Score 15.6; DB 9; Length 25;
Best Local Similarity 36.4%; Pred. No. 2.1e+04;
Matches 8; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
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```
QY 54 GCUUUGUCUCUGUUUCUGGAU 75
Db 25 GCTTTGATTGAGTGTCTGGAT 4
```

RESULT 12

```
US-11-348-413-414080/c
; Sequence 414080, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 414080
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 12552; WAN01UOO2; Start 495; Stop 519;
; OTHER INFORMATION: 00000000011111
US-11-348-413-414080
```

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Query Match      18.4%; Score 15.6; DB 9; Length 25;
Best Local Similarity 36.4%; Pred. No. 2.1e+04;
Matches 8; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
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```
QY 54 GCUUUGUCUCUGUUUCUGGAU 75
Db 24 GCTTTGATTGAGTGTCTGGAT 3
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RESULT 13

```
US-11-348-413-884139/c
; Sequence 884139, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 884139
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 7816; WAN01UMPL_at; Start 185; Stop 209;
; OTHER INFORMATION: 000000010000000
US-11-348-413-884139
```

```
Query Match      18.4%; Score 15.6; DB 9; Length 25;
Best Local Similarity 36.4%; Pred. No. 2.1e+04;
Matches 8; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
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Query Match 18.1%; Score 15.4; DB 9; Length 25;
Best Local Similarity 40.0%; Pred. No. 2.5e+04;
Matches 10; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
QY 52 GCGCUUUGCUUGCUUUGCUUGGAUG 76
DB 25 GAGCTTAAGTCTGTGTGGCATG 1

Search completed: October 16, 2006, 14:22:02
Job time : 189.534 secs

QY 54 GCUUGCUUGCUUGCUUGCUUGGAU 75
DB 25 GATTGGCCTCTGTTTCTTGAT 4
RESULT 14
US-11-217-529-98618/c
; Sequence 98618, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 98618
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-98618

Query Match 18.1%; Score 15.4; DB 8; Length 25;
Best Local Similarity 52.0%; Pred. No. 2.5e+04;
Matches 13; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
QY 60 CUUCUUGCUUGCUUGCUUGGACUCC 84
DB 25 CTTCAAAATTCGACGACGATGCC 1

RESULT 15
US-11-348-413-350690/c
; Sequence 350690, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 350690
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 10828; WAN01UOXH; Start 36; Stop 60;
; OTHER INFORMATION: 00000000011101
US-11-348-413-350690

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 13:53:09 ; Search time 125.594 Seconds
(without alignments)
1332.341 Million cell updates/sec

Title: US-10-604-726A-6034

Perfect score: 24
Sequence: 1 ugagagggcgguuagcgucc 24

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 4443654

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*
15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.8	65.8	24	6 ABQ11002	Abq11002 Oligonuc
2	15.8	65.8	24	6 ABQ04674	Abq04674 Oligonuc
3	15.8	65.8	24	6 ABQ04715	Abq04715 Oligonuc
4	15.8	65.8	24	6 ABQ00358	Abq00358 Oligonuc
5	15.8	65.8	24	6 ABQ11043	Abq11043 Oligonuc
6	15.8	65.8	25	6 ABQ12538	Abq12538 Oligonuc
7	15.8	65.8	25	6 ABQ12579	Abq12579 Oligonuc
8	15.2	63.3	28	2 AAT74315	Aat74315 PCR prime
9	14.6	60.8	24	6 AAL50117	Aal50117 Human CAB
10	14.4	60.0	21	9 ADA24254	Ada24254 Major all
11	14.2	59.2	20	14 ADZ97885	Adz97885 Human ant
12	14.2	59.2	21	11 ADJ13347	Adj13347 Human DNA
13	14.2	59.2	25	3 AAAG1591	Aaag1591 Human Tes
14	14	58.3	25	9 ACT82777	Act82777 Human mic
15	13.8	57.5	17	8 ACDS57816	Acd57816 HCV DNaz
16	13.8	57.5	17	12 ADI83268	Adi83268 HCV DNaz
17	13.8	57.5	22	2 AAT47817	Aat47817 PCR prime
18	13.8	57.5	22	2 AAX04299	Aax04299 Mouse neu

19	13.6	56.7	21	14 ACL41634	ACL41634 CACNA1D s
20	13.6	56.7	21	14 ACL41632	ACL41632 CACNA1D t
21	13.6	56.7	21	14 ACL43064	ACL43064 CACNA1D s
22	13.6	56.7	30	14 AED57579	Aed57579 Human ost
23	13.4	55.8	28	6 ABQ79069	Abq79069 Rat ZAO r
24	13.4	55.8	28	6 ABL50688	AbL50688 Rat G pro
25	13.4	55.8	28	10 ADD69148	Add69148 Angiogene
26	13.4	55.8	30	4 AAS95201	Aas95201 Otoferrin
27	13.2	55.0	19	14 AEA25301	Aea25301 Anti-myos
28	13.2	55.0	19	14 AEA25458	Aea25458 Anti-myos
29	13.2	55.0	20	10 ABZ99113	Abz99113 Human PDE
30	13.2	55.0	20	11 ABD32144	Abd32144 Human PDE
31	13.2	55.0	20	12 ADJ60998	Adj60998 Oligonuc
32	13.2	55.0	20	12 ADO46487	Ado46487 Human Oli
33	13.2	55.0	20	14 ADZ97886	Adz97886 Human ant
34	13.2	55.0	20	14 AED42052	Aed42052 Antisense
35	13.2	55.0	21	11 ADJ13385	Adj13385 Human DNA
36	13.2	55.0	21	13 ADU43508	Adu43508 Knock-dow
37	13.2	55.0	25	5 AAF85432	Aaf85432 PCR prime
38	13.2	55.0	25	9 ACK10389	Ack10389 Human mic
39	13.2	55.0	25	10 AAD64634	Aad64634 Rat tauri
40	13.2	55.0	25	12 ADO61007	Ado61007 Human deb
41	13.2	55.0	25	14 AEC90171	Aec90171 CYP2D6 ge
42	13.2	55.0	26	13 ADZ15690	Adz15690 Mutagenic
43	13.2	55.0	26	13 ADZ15691	Adz15691 Mutagenic
44	13.2	55.0	26	14 ADW95301	Adw95301 Upstream
45	13.2	55.0	30	2 AAQ89038	Aaq89038 VEGF 2'-N

ALIGNMENTS

RESULT 1
ABQ11002
ID ABQ11002 standard; DNA; 24 BP.

AC ABQ11002;

DT 11-JUN-2002 (first entry)

DE Oligonucleotide adapter/capture probe 10993.

KW Oligonucleotide array; adapter sequence; probe; ss.

OS Synthetic.

PN WO200216649-A2.

PD 28-FEB-2002.

PF 27-AUG-2001; 2001WO-US026519.

PR 25-AUG-2000; 2000US-0227948P.

PR 29-AUG-2000; 2000US-0228854P.

XX (ILLU-) ILLUMINA INC.

XX Gunderson K;

XX WPI; 2002-292068/33.

PT Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.

XX Claim 1; Page 225; 261pp; English.

XX The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid

CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid

XX SQ Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 65.8%; Score 15.8; DB 6; Length 24;

Best Local Similarity 73.7%; Pred. No. 1.3e+03;

Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAGAGGGCGUGUUAAGGC 20

||||| | : : : :
Db 4 GAGAGGCGTGGTTAAGGC 22

RESULT 2

ABQ04674

ID ABQ04674 standard; DNA; 24 BP.

XX AC ABQ04674;

XX DT 11-JUN-2002 (first entry)

XX Oligonucleotide adapter/capture probe 4665.

XX Oligonucleotide array; adapter sequence; probe; ss.

XX Synthetic.

XX PN WO200216649-A2.

XX PD 28-FEB-2002.

XX PF 27-AUG-2001; 2001WO-US026519.

XX PR 25-AUG-2000; 2000US-0227948P.

XX PR 29-AUG-2000; 2000US-0228854P.

XX PA (ILLU-) ILLUMINA INC.

XX PI Gunderson K;

XX WPI; 2002-292068/33.

XX Array comprising adapter sequences useful for immobilizing or detecting a

XX target nucleic acid sequence, has different addresses comprising

XX different specific capture probes.

XX Claim 1; Page 147; 261pp; English.

XX The invention relates to an oligonucleotide array (I) comprising at least

XX 25 different addresses (adapter sequences) with each comprising a

XX different capture probe selected from a group consisting of the sequences

XX given in ABQ0010-ABQ13409. (I) is useful for immobilising a target

XX nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-

XX ABQ13409) to a target nucleic acid to form a modified target nucleic acid

XX and contacting the modified target nucleic acid with (I). The steps of

XX above method is useful for detecting a target nucleic acid, which further

XX comprises detecting the presence of the modified target nucleic acid

XX SQ Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 65.8%; Score 15.8; DB 6; Length 24;

Best Local Similarity 73.7%; Pred. No. 1.3e+03;

Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAGAGGGCGUGUUAAGGC 20

||||| | : : : :
Db 4 GAGAGGCGTGGTTAAGGC 22

RESULT 3

ABQ04715/c

ID ABQ04715 standard; DNA; 24 BP.

XX AC ABQ04715;

XX DT 11-JUN-2002 (first entry)

XX Oligonucleotide adapter/capture probe 4706.

XX Oligonucleotide array; adapter sequence; probe; ss.

XX Synthetic.

XX PN WO200216649-A2.

XX PD 28-FEB-2002.

XX PF 27-AUG-2001; 2001WO-US026519.

XX PR 25-AUG-2000; 2000US-0227948P.

XX PR 29-AUG-2000; 2000US-0228854P.

XX PA (ILLU-) ILLUMINA INC.

XX PI Gunderson K;

XX WPI; 2002-292068/33.

XX Array comprising adapter sequences useful for immobilizing or detecting a

XX target nucleic acid sequence, has different addresses comprising

XX different specific capture probes.

XX Claim 1; Page 147; 261pp; English.

XX The invention relates to an oligonucleotide array (I) comprising at least

XX 25 different addresses (adapter sequences) with each comprising a

XX different capture probe selected from a group consisting of the sequences

XX given in ABQ0010-ABQ13409. (I) is useful for immobilising a target

XX nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-

XX ABQ13409) to a target nucleic acid to form a modified target nucleic acid

XX and contacting the modified target nucleic acid with (I). The steps of

XX above method is useful for detecting a target nucleic acid, which further

XX comprises detecting the presence of the modified target nucleic acid

XX SQ Sequence 24 BP; 5 A; 10 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 65.8%; Score 15.8; DB 6; Length 24;

Best Local Similarity 73.7%; Pred. No. 1.3e+03;

Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAGAGGGCGUGUUAAGGC 20

||||| | : : : :
Db 21 GAGAGGCGTGGTTAAGGC 3

RESULT 4

ABQ00358

ID ABQ00358 standard; DNA; 24 BP.

XX AC ABQ00358;

XX DT 11-JUN-2002 (first entry)

XX Oligonucleotide adapter/capture probe 349.

XX Oligonucleotide array; adapter sequence; probe; ss.

XX Synthetic.

XX PN WO200216649-A2.

XX PD 28-FEB-2002.

XX PF 27-AUG-2001; 2001WO-US026519.


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XX 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX (ILLU-) ILLUMINA INC.
XX Gunderson K;
XX WPI; 2002-292068/33.
XX Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX Claim 1; Page 52; 261pp; English.
XX The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
XX Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;
Query Match 65.8%; Score 15.8; DB 6; Length 24;
Best Local Similarity 73.7%; Pred. NO. 1.3e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
XX 2 GAGAGGGCGUGGUUAGGC 20
DB ||||| | :||:||||
4 GAGAGGCGTTGGTTAAGGC 22
||| | :||:||||

RESULT 5
ABQ11043/C
ID ABQ11043 standard; DNA; 24 BP.
XX
XX ABQ11043;
XX
XX 11-JUN-2002 (first entry)
XX Oligonucleotide adapter/capture probe 11034.
XX Oligonucleotide array; adapter sequence; probe; ss.
XX Synthetic.
XX WO200216649-A2.
XX
XX 28-FEB-2002.
XX
XX 27-AUG-2001; 2001WO-US026519.
XX
XX 25-AUG-2000; 2000US-0227948P.
XX 29-AUG-2000; 2000US-0228854P.
XX (ILLU-) ILLUMINA INC.
XX Gunderson K;
XX WPI; 2002-292068/33.
XX Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX Claim 1; Page 225; 261pp; English.
XX The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
XX Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;
Query Match 65.8%; Score 15.8; DB 6; Length 24;
Best Local Similarity 73.7%; Pred. NO. 1.3e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
XX 2 GAGAGGGCGUGGUUAGGC 20
DB ||||| | :||:||||
4 GAGAGGCGTTGGTTAAGGC 22
||| | :||:||||

RESULT 6
ABQ12538
ID ABQ12538 standard; DNA; 25 BP.
XX
XX ABQ12538;
XX
XX 11-JUN-2002 (first entry)
XX Oligonucleotide adapter/capture probe 12529.
XX Oligonucleotide array; adapter sequence; probe; ss.
XX Synthetic.
XX WO200216649-A2.
XX
XX 28-FEB-2002.
XX
XX 27-AUG-2001; 2001WO-US026519.
XX
XX 25-AUG-2000; 2000US-0227948P.
XX 29-AUG-2000; 2000US-0228854P.
XX (ILLU-) ILLUMINA INC.
XX Gunderson K;
XX WPI; 2002-292068/33.
XX Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX Claim 1; Page 244; 261pp; English.
XX The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
XX Sequence 25 BP; 7 A; 2 C; 10 G; 6 T; 0 U; 0 Other;
Query Match 65.8%; Score 15.8; DB 6; Length 25;
Best Local Similarity 73.7%; Pred. NO. 1.3e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
XX 2 GAGAGGGCGUGGUUAGGC 20
DB ||||| | :||:||||
```

```
Db          5 GAGAGGCGTTGGTTAAGGC 23
RESULT 7
ABQ12579/c
ID ABQ12579 standard; DNA; 25 BP.
XX
AC ABQ12579;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 12570.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
OS Synthetic.
XX
XX WO200216649-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026519.
XX
PR 25-AUG-2000; 2000US-0227948P.
XX
PR 29-AUG-2000; 2000US-0228854P.
XX
XX (ILLU-) ILLUMINA INC.
XX
XX Gunderson K;
XX
XX WPI; 2002-292068/33.
XX
XX Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
XX Claim 1; Page 244; 261pp; English.
XX
XX The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
XX Sequence 25 BP; 5 A; 10 C; 2 G; 8 T; 0 U; 0 Other;
XX
Query Match 65.8%; Score 15.8; DB 6; Length 25;
Best Local Similarity 73.7%; Pred. No. 1.3e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
QY 2 GAGAGGCGCGUGUUAAGGC 20
||||| : : : : :
Db 22 GAGAGGCGTTGGTTAAGGC 4
||||| : : : : :
RESULT 8
AAT74315/c
ID AAT74315 standard; DNA; 28 BP.
XX
AC AAT74315;
XX
DT 09-FEB-1998 (first entry)
XX
DE PCR primer JC25.2.
XX
XX Cleaning; bleaching; cellulose; fabric; enzyme hybrid; peroxidase;
KW cellulose binding domain; Humicola insolens; cellulase;
KW Coprinus cinereus; laccase; plaamid pJC25; PCR; primer; ss.
XX
XX
OS Synthetic.
OS Corynascus heterothallicus.
XX
XX WO9728243-A1.
XX
XX 07-AUG-1997.
XX
XX 29-JAN-1997; 97WO-DK000042.
XX
XX 29-JAN-1996; 96DK-00000094.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Von Der Osten C, Cherry JR, Bjornvad M, Vind J, Rasmussen M;
XX WPI; 1997-402598/37.
XX
XX Cleaning of cellulosic fabrics - using an enzyme hybrid comprising a
PT sequence of a non-cellulolytic enzyme linked to a cellulose-binding
PT domain sequence.
XX
XX Example 6; Page 85; 124pp; English.
XX
XX PCR primers Cippcrdwn (AAT74310) and JC25.2 (AAT74315) were used to
CC amplify a DNA fragment encoding the entire laccase protein (residues 1-
CC 620) of Myceliophthora thermophila plus 232 bp of upstream sequence,
CC using plaamid pJRC30 as template. The PCR product was ligated to a DNA
CC fragment encoding the Humicola insolens family 45 cellulase linker domain
CC (35 amino acids), the H. insolens family 45 cellulase cellulose binding
CC domain (CBD, 37 amino acids) plus 20 bp of 3'-noncoding sequences in
CC vector pJC106 to obtain plaamid pJC25 (see AAT74282). A claimed process
CC for removal or bleaching of soiling or stains on a cellulosic fabric
CC comprises contacting the fabric with a modified enzyme (enzyme hybrid)
CC comprising a catalytically active portion of a non-cellulolytic enzyme
CC linked to a CBD. The hybrid enzyme gives improved enzyme performance by
CC increasing the affinity of the enzyme for the fabric
XX
XX Sequence 28 BP; 3 A; 15 C; 5 G; 5 T; 0 U; 0 Other;
XX
Query Match 63.3%; Score 15.2; DB 2; Length 28;
Best Local Similarity 75.0%; Pred. No. 2.5e+03;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
XX
QY 2 GAGAGGCGCGUGUUAAGGC 21
||||| : : : : :
Db 20 GCGAGTGGCTGCTCAGGCG 1
||||| : : : : :
RESULT 9
AAL50117/c
ID AAL50117 standard; DNA; 24 BP.
XX
XX AAL50117;
XX
XX 28-JAN-2003 (first entry)
XX
XX Human CAB55953-1 ligand binding domain PCR primer #2.
XX
XX Human; CAB55953.1; nuclear hormone receptor ligand binding domain; LBDG3;
KW cancer; autoimmune disorder; inflammation; PCR; antiseborrheic;
KW dermatological; anti-HIV; neuroprotective; nephrotropic; antitanginal;
KW tranquilizer; antiarrhythmic; antiarteriosclerotic; antiaesthetic;
KW immunosuppressive; virucide; fungicide; antibacterial; antiparasitic;
KW cardiant; antidepressant; antidiabetic; vasotropic; antiinflammatory;
KW nephrotropic; cytostatic; antilipemic; hypotensive; antiallergic;
KW antithyroid; anorectic; osteopathic; analgesic; antipsoriatic; vulnary;
KW cerebroprotective; haemostatic; thrombolytic; cardiovascular disorder;
KW neurological disorder; infection; primer; ss.
XX
XX Homo sapiens.
OS
XX WO200270557-A2.
XX
XX
```

PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-GB000937.
XX
PR 05-MAR-2001; 2001GB-00005402.
XX
PA (INPH-) INPHARMATICA LTD.
XX
PI Fagan RJ, Phelps CB, Phillips T, Pierron VN, Allen KE, Allen JM;
PI Potter SJ;
XX
XX WPI; 2002-698731/75.
XX
XX New CAB55953.1 or LBDG3 polypeptide, useful as a nuclear hormone receptor
PT ligand-binding domain, or for manufacturing of a medicament for
PT diagnosing or treating cell proliferative disorders or
PT autoimmune/inflammatory disorders.
XX
PS Example 2; Page 64; 122pp; English.
XX
CC The present invention relates to the protein and coding sequences of a
CC human nuclear hormone receptor ligand binding domain designated
CC CAB55953.1 or LBDG3. The sequences are useful in the treatment of cancer,
CC autoimmune/inflammatory disorders, including allergy, inflammatory bowel
CC disease, arthritis, psoriasis and respiratory tract inflammation, asthma
CC and organ transplant rejection, cardiovascular disorders, including
CC hypertension, oedema, angina, atherosclerosis, thrombosis, sepsis, shock,
CC reperfusion injury, heart arrhythmia, and ischaemia, neurological
CC disorders including central nervous system disease, Alzheimer's disease,
CC brain injury, stroke, amyotrophic lateral sclerosis, anxiety, depression
CC and pain, developmental disorders, metabolic disorders including diabetes
CC mellitus, osteoporosis, lipid metabolism disorders, hyperthyroidism,
CC hyperparathyroidism, hypercalcaemia, hypercholesterolaemia,
CC hyperlipidaemia and obesity, renal disorders including
CC glomerulonephritis, renovascular hypertension, dermatological disorders
CC including acne, eczema and wound healing, negative effects of aging,
CC acquired immunodeficiency syndrome (AIDS), viral, bacterial, fungal and
CC parasitic infections, and other pathological conditions, particularly
CC those in which nuclear hormone receptors are implicated. The present
CC sequence is a PCR primer used to isolate the coding sequence of the
CC invention
XX
XX Sequence 24 BP; 7 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
SQ
Query Match 60.8%; Score 14.6; DB 6; Length 24;
Best Local Similarity 61.9%; Pred. No. 4.8e+03;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 3 AGAGGGGCGUUAAGCGUC 23
DB 23 AGAGGGGCTTATTAACTCGTC 3
RESULT 10
ADA245454/c
ID ADA2454 standard; DNA; 21 BP.
XX
AC ADA2454;
XX
DT 20-NOV-2003 (first entry)
XX
DE Major allergenic storage protein FAGAG1 PCR primer FAG19 SEQ ID NO:7.
XX food testing; allergen; PCR primer; *Fagopyrum esculentum*;
KW major allergenic storage protein; FAGAG1; ss.
XX
OS Synthetic.
OS *Fagopyrum esculentum*.
XX
XX WO2003068964-A1.
XX
XX 21-AUG-2003.
PD
XX

PF 26-SEP-2002; 2002WO-JP009982.
XX
PR 15-FEB-2002; 2002JP-00038930.
XX
PA (NISS) NISSHIN SEIFUN GROUP INC.
XX
XX Yamakawa H, Suzuki E, Miyatake K, Hayakawa K;
PI WPI; 2003-637145/60.
XX
XX PCR-based method for testing foods using specific primers designed from
PT genes of target substance, useful in detecting trace components or
PT identifying specific harmful allergens in (processed) foods.
XX
PS Disclosure; Page 10; 38pp; Japanese.
XX
CC The present invention describes a method for testing the presence or
CC absence of a specific substance in a food by performing PCR with primers
CC which are designed on the basis of data obtained from a part of a gene of
CC the specific substance. Also described: (1) a similar method for
CC detecting a trace component contained in a food, or for identifying a
CC harmful allergen specific to a consumer of such substance by performing
CC PCR with primers which are designed on the basis of data obtained from a
CC part of a gene of the specific substance; (2) primers for PCR applicable
CC in food testing which are designed on the basis of data obtained from a
CC part of a gene of the specific substance; and (3) kits for determining
CC concentration of a specific substance in the food containing the primers.
CC The methods are useful for testing foods, which can be used in detecting
CC trace components or identifying specific harmful allergens in (processed)
CC foods, particularly applicable in food safety and management. The present
CC sequence represents a PCR primer for a *Fagopyrum esculentum* major
CC allergenic storage protein designated FAGAG1, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 60.0%; Score 14.4; DB 9; Length 21;
Best Local Similarity 68.8%; Pred. No. 5.9e+03;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 7 GGGCGUGUUAAGCGU 22
DB 17 GGGCTGGTTATGCGGT 2
RESULT 11
ADZ97885/c
ID ADZ97885 standard; DNA; 20 BP.
XX
AC ADZ97885;
XX
DT 28-JUL-2005 (first entry)
XX
DE Human antisense oligonucleotide SEQ ID NO:39.
XX protein interaction; antisense oligonucleotide; ss.
KW
XX Homo sapiens.
OS
XX US2005112118-A1.
XX
XX 26-MAY-2005.
XX
XX 20-OCT-2003; 2003US-00690276.
XX
XX 02-DEC-1999; 99US-0168377P.
PR 02-DEC-1999; 99US-0168379P.
PR 25-FEB-2000; 2000US-0185056P.
PR 01-DEC-2000; 2000US-00727384.
PR 14-DEC-2000; 2000US-0255063P.
PR 21-DEC-2000; 2000US-0256986P.
PR 04-JAN-2001; 2001US-0259571P.
PR 04-JAN-2001; 2001US-0259572P.
PR

PT Trypsin family serine proteases expressed specifically in mature testis
PT for development of methods for diagnosis and treatment of sterility and
PT for contraception.

XX Example 9; Page 45; 121pp; Japanese.

XX The invention relates to novel murine and human testis specific serine
CC proteases (Tespac PRO; AAB03156-B03160) and to cDNAs encoding them
CC (AAA61558-A61562). It also encompasses expression vectors and host cells
CC comprising a nucleotide sequence encoding a protease of the invention,
CC inhibitors of the proteases and antibodies against the proteases. The
CC novel proteases are members of the trypsin family of serine proteases,
CC having the serine and histidine active site signatures characteristic of
CC this family. The proteases are specifically expressed in mature testis
CC and participate in the differentiation and maturation of sperm. The
CC proteases are potentially useful for the development of pharmaceuticals
CC for the treatment of male infertility and other male reproductive
CC disorders, and for the development of contraceptives. They may also be
CC used as reagents for the diagnosis of male infertility. Sequences
CC AAA61590-A61593 represent RACE (rapid amplification of cDNA ends) PCR
CC primers used in the isolation of cDNA encoding human Tespac PRO-3
CC (AAA61561).

XX Sequence 25 BP; 4 A; 2 C; 10 G; 9 T; 0 U; 0 Other;

Query Match 59.2%; Score 14.2; DB 3; Length 25;
Best Local Similarity 63.2%; Pred. No. 7.4e+03;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 GAGGGCGUGGUUAGGCGU 22

DB 3 GATGGCGTAGTTAAGTCGT 21

RESULT 14

ACT182777
ID AC182777 standard; DNA; 25 BP.

AC AC182777;

DT 14-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 82769.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.

XX Homo sapiens.

OS US200310410-A1.

PN 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

PF 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

PA Mittmann MP;

PI WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 82768; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.

CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 6 A; 4 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 9; Length 25;
Best Local Similarity 59.1%; Pred. No. 9.2e+03;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 2 GAGAGGGCGUGGUUAGGCGUC 23

DB 1 GACAGGGGATCGTTAGACGTC 22

RESULT 15

ACD57816/C

ID ACD57816 standard; RNA; 17 BP.

XX ACD57816;

DT 23-SEP-2003 (first entry)

XX HCV DNAzyme substrate sequence #514.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.

OS Hepatitis C virus.

PN WO200281494-A1.

XX 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.

XX 08-JUN-2001; 2001US-00877478.

XX 08-JUN-2001; 2001US-0296876P.

XX 24-OCT-2001; 2001US-0330505P.

XX 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MACE/) MACEJAK D.

PA (MCSW/) MCSWIGGEN J.

PA (MORR/) MORRISSEY D.

PA (PAVC/) PAVCO P.

PA (LEEP/) LEE P.

PA (DRAP/) DRAPER K.

PA (ROBE/) ROBERTS E.
XX
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX
DR WPI; 2003-229207/22.
XX
XX Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
XX Claim 1; Page 243; 387pp; English.
PS
XX The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, ambezymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HCV
CC DNazyme or minus strand DNazyme sequences disclosed in the present
XX invention
SQ Sequence 17 BP; 4 A; 9 C; 1 G; 0 T; 3 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 8; Length 17;
Best Local Similarity 70.6%; Pred. No. 1.1e+04;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGGGCGUUAAGCGU 22
Db 17 GGGGCGAGGTTAAGGTGT 1

Search completed: October 16, 2006, 14:15:57
Job time : 126.594 secs

GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 13:57:30 ; Search time 590.797 Seconds
(without alignments)
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Title: US-10-604-726A-6034

Perfect score: 24
Sequence: 1 ugagagggcgguuaagcgucc 24

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 1796954

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_env:*
2: gb_pat:*
3: gb_ph:*
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6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.8	65.8	24	2	AX443910 Sequence
2	15.8	65.8	25	2	AX447886 Sequence
3	14.6	60.8	24	2	AX538707 Sequence
4	13.8	57.5	22	2	AR036420 Sequence
5	13.8	57.5	22	2	I29861 Sequence 12
6	13.4	55.8	28	2	BD141786 Novel G p
7	13.4	55.8	28	2	BD173668 Novel phy
8	13.4	55.8	28	2	BD181737 Novel G p
9	13.2	55.0	25	2	AR148541 Sequence
10	13.2	55.0	25	2	I62320 Sequence 23
11	13	54.2	17	2	AX215297 Sequence
12	13	54.2	17	2	AX215298 Sequence
13	13	54.2	17	2	AX215299 Sequence
14	13	54.2	17	2	AX215300 Sequence
15	13	54.2	20	2	AX298773 Sequence
16	13	54.2	27	2	AX347840 Sequence
17	12.8	53.3	19	2	AR069252 Sequence
18	12.8	53.3	19	2	CS101953 Sequence

19	12.8	53.3	19	2	CS102090	CS102090 Sequence
20	12.8	53.3	25	2	AR240243	AR240243 Sequence
21	12.6	52.5	19	2	AR628705	AR628705 Sequence
22	12.6	52.5	20	2	AR100388	AR100388 Sequence
23	12.6	52.5	20	2	AR150043	AR150043 Sequence
24	12.6	52.5	20	2	BD227916	BD227916 Antisense
25	12.6	52.5	20	2	AR442443	AR442443 Sequence
26	12.6	52.5	20	8	AB213914	AB213914 Synthetic
27	12.6	52.5	21	2	AR231257	AR231257 Sequence
28	12.6	52.5	22	2	CS020856	CS020856 Sequence
29	12.6	52.5	25	2	AR404657	AR404657 Sequence
30	12.6	52.5	26	5	S75471	S75471 rhodopsin {
31	12.6	52.5	27	2	DD210483	DD210483 GENOMIC S
32	12.6	52.5	28	2	AR534679	AR534679 Sequence
33	12.6	52.5	28	2	AX004269	AX004269 Sequence
34	12.6	52.5	30	2	AR139887	AR139887 Sequence
35	12.6	52.5	30	2	AR139924	AR139924 Sequence
36	12.6	52.5	30	2	AR167531	AR167531 Sequence
37	12.6	52.5	30	2	AR167568	AR167568 Sequence
38	12.6	52.5	30	2	AX924030	AX924030 Sequence
39	12.6	52.5	30	2	BD084559	BD084559 Recombina
40	12.6	52.5	30	2	BD084596	BD084596 Recombina
41	12.6	52.5	30	2	BD250400	BD250400 Methode f
42	12.6	52.5	30	2	AR234255	AR234255 Sequence
43	12.6	52.5	30	2	AR234292	AR234292 Sequence
44	12.6	52.5	30	2	AR238589	AR238589 Sequence
45	12.6	52.5	30	2	AR476172	AR476172 Sequence

ALIGNMENTS

RESULT 1	AX443910	Sequence 365 from Patent WO0216649.	24 bp	DNA	linear	PAT 03-JUL-2002
LOCUS	AX443910					
DEFINITION	AX443910					
ACCESSION	AX443910.1	GI:21691188				
VERSION	AX443910.1	GI:21691188				
KEYWORDS	synthetic construct					
SOURCE	synthetic construct					
ORGANISM	other sequences; artificial sequences.					
REFERENCE	1					
AUTHORS	Gunderson,K.					
TITLE	Probes and decoder oligonucleotides					
JOURNAL	Patent: WO 0216649-A 365 28-FEB-2002;					
ILLUMINA, INC. (US)						
FEATURES	Location/Qualifiers					
source	1..24					
	/organism="synthetic construct"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:32630"					
	/note="Computer Generated Probe Sequence."					

ORIGIN

Query Match	65.8%;	Score 15.8;	DB 2;	Length 24;
Best Local Similarity	73.7%;	Pred. NO. 6.2e+04;		
Matches	14;	Conservative	3;	Mismatches 2;
				Indels 0;
				Gaps 0;
Qy	2	GAGAGGGCGUGUUAAGGC	20	
Db	4	GAGAGGGCGTTGGTTAAGGC	22	
RESULT 2	AX447886			
LOCUS	AX447886	Sequence 4341 from Patent WO0216649.	25 bp	DNA
DEFINITION	AX447886			
ACCESSION	AX447886.1	GI:21696785		
VERSION	AX447886.1	GI:21696785		
KEYWORDS				
SOURCE	synthetic construct			
ORGANISM	synthetic construct			

other sequences; artificial sequences.		/mol_type="unassigned DNA"	
REFERENCE	1	Query Match	57.5%; Score 13.8; DB 2; Length 22;
AUTHORS	Gunderson,K.	Best Local Similarity	70.6%; Pred. No. 5.4e+05;
TITLE	Probes and decoder oligonucleotides	Matches 12; Conservative	3; Mismatches 2; Indels 0; Gaps 0;
JOURNAL	Patent: WO 0216649-A 4341 28-FEB-2002;		
FEATURES	Illumina, Inc. (US)		
source	Location/Qualifiers		
	1..25		
	/organism="synthetic construct"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:32630"		
	/note="Computer Generated Probe Sequence."		
ORIGIN			
Query Match	65.8%; Score 15.8; DB 2; Length 25;		
Best Local Similarity	73.7%; Pred. No. 6.1e+04;		
Matches 14; Conservative	3; Mismatches 2; Indels 0; Gaps 0;		
QY	2 GAGAGGGCGUGGUUAGGC 20		
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Db	5 GAGAGGCGTGGTTAAGC 23		
RESULT 3			
AX538707/c			
LOCUS	Sequence 6 from Patent WO02070557.		
DEFINITION	24 bp DNA linear PAT 23-NOV-2002		
ACCESSION	AX538707		
VERSION	AX538707.1 GI:25271321		
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	other sequences; artificial sequences.		
REFERENCE	1		
AUTHORS	Fagan,R.J., Phelps,C.B., Phillips,T., Pierron,V.N., Allen,K.E., Allen,J.M. and Potter,S.J.		
TITLE	Nuclear hormone receptor ligand binding domain		
JOURNAL	Patent: WO 02070557-A 6 12-SEP-2002;		
FEATURES	Inpharmatica Limited (GB)		
source	Location/Qualifiers		
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ORIGIN			
Query Match	60.8%; Score 14.6; DB 2; Length 24;		
Best Local Similarity	61.9%; Pred. No. 2.3e+05;		
Matches 13; Conservative	4; Mismatches 4; Indels 0; Gaps 0;		
QY	3 AGAGGGCGUGGUAGGCUC 23		
	: : : :		
Db	23 AGAGGGCGTTATTAACTGTC 3		
RESULT 4			
AR036420/c			
LOCUS	Sequence 12 from patent US 5872214.		
DEFINITION	22 bp DNA linear PAT 29-SEP-1999		
ACCESSION	AR036420		
VERSION	AR036420.1 GI:5953088		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 22)		
AUTHORS	Seizinger,B.R., Kley,N.A. and Bianchi,A.B.		
TITLE	NF2 isoforms		
JOURNAL	Patent: US 5872214-A 12 16-FEB-1999;		
FEATURES	Location/Qualifiers		
source	1..22		
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other sequences; artificial sequences.		/mol_type="unassigned DNA"	
REFERENCE	1	Query Match	57.5%; Score 13.8; DB 2; Length 22;
AUTHORS	Gunderson,K.	Best Local Similarity	70.6%; Pred. No. 5.4e+05;
TITLE	Probes and decoder oligonucleotides	Matches 12; Conservative	3; Mismatches 2; Indels 0; Gaps 0;
JOURNAL	Patent: WO 0216649-A 4341 28-FEB-2002;		
FEATURES	Illumina, Inc. (US)		
source	Location/Qualifiers		
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	/db_xref="taxon:32630"		
	/note="Computer Generated Probe Sequence."		
ORIGIN			
Query Match	65.8%; Score 15.8; DB 2; Length 25;		
Best Local Similarity	73.7%; Pred. No. 6.1e+04;		
Matches 14; Conservative	3; Mismatches 2; Indels 0; Gaps 0;		
QY	2 GAGAGGGCGUGGUUAGGC 20		
	: : : :		
Db	5 GAGAGGCGTGGTTAAGC 23		
RESULT 3			
AX538707/c			
LOCUS	Sequence 6 from Patent WO02070557.		
DEFINITION	24 bp DNA linear PAT 23-NOV-2002		
ACCESSION	AX538707		
VERSION	AX538707.1 GI:25271321		
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	other sequences; artificial sequences.		
REFERENCE	1		
AUTHORS	Fagan,R.J., Phelps,C.B., Phillips,T., Pierron,V.N., Allen,K.E., Allen,J.M. and Potter,S.J.		
TITLE	Nuclear hormone receptor ligand binding domain		
JOURNAL	Patent: WO 02070557-A 6 12-SEP-2002;		
FEATURES	Inpharmatica Limited (GB)		
source	Location/Qualifiers		
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	/note="LBDG3 Reverse primer"		
ORIGIN			
Query Match	60.8%; Score 14.6; DB 2; Length 24;		
Best Local Similarity	61.9%; Pred. No. 2.3e+05;		
Matches 13; Conservative	4; Mismatches 4; Indels 0; Gaps 0;		
QY	3 AGAGGGCGUGGUAGGCUC 23		
	: : : :		
Db	23 AGAGGGCGTTATTAACTGTC 3		
RESULT 4			
AR036420/c			
LOCUS	Sequence 12 from patent US 5872214.		
DEFINITION	22 bp DNA linear PAT 29-SEP-1999		
ACCESSION	AR036420		
VERSION	AR036420.1 GI:5953088		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 22)		
AUTHORS	Seizinger,B.R., Kley,N.A. and Bianchi,A.B.		
TITLE	NF2 isoforms		
JOURNAL	Patent: US 5872214-A 12 16-FEB-1999;		
FEATURES	Location/Qualifiers		
source	1..22		
	/organism="unknown"		

other sequences; artificial sequences.		/mol_type="unassigned DNA"	
REFERENCE	1	Query Match	57.5%; Score 13.8; DB 2; Length 22;
AUTHORS	Gunderson,K.	Best Local Similarity	70.6%; Pred. No. 5.4e+05;
TITLE	Probes and decoder oligonucleotides	Matches 12; Conservative	3; Mismatches 2; Indels 0; Gaps 0;
JOURNAL	Patent: WO 0216649-A 4341 28-FEB-2002;		
FEATURES	Illumina, Inc. (US)		
source	Location/Qualifiers		
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	/organism="synthetic construct"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:32630"		
	/note="Computer Generated Probe Sequence."		
ORIGIN			
Query Match	65.8%; Score 15.8; DB 2; Length 25;		
Best Local Similarity	73.7%; Pred. No. 6.1e+04;		
Matches 14; Conservative	3; Mismatches 2; Indels 0; Gaps 0;		
QY	2 GAGAGGGCGUGGUUAGGC 20		
	: : : :		
Db	5 GAGAGGCGTGGTTAAGC 23		
RESULT 3			
AX538707/c			
LOCUS	Sequence 6 from Patent WO02070557.		
DEFINITION	24 bp DNA linear PAT 23-NOV-2002		
ACCESSION	AX538707		
VERSION	AX538707.1 GI:25271321		
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	other sequences; artificial sequences.		
REFERENCE	1		
AUTHORS	Fagan,R.J., Phelps,C.B., Phillips,T., Pierron,V.N., Allen,K.E., Allen,J.M. and Potter,S.J.		
TITLE	Nuclear hormone receptor ligand binding domain		
JOURNAL	Patent: WO 02070557-A 6 12-SEP-2002;		
FEATURES	Inpharmatica Limited (GB)		
source	Location/Qualifiers		
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	/mol_type="unassigned DNA"		
	/db_xref="taxon:32630"		
	/note="LBDG3 Reverse primer"		
ORIGIN			
Query Match	60.8%; Score 14.6; DB 2; Length 24;		
Best Local Similarity	61.9%; Pred. No. 2.3e+05;		
Matches 13; Conservative	4; Mismatches 4; Indels 0; Gaps 0;		
QY	3 AGAGGGCGUGGUAGGCUC 23		
	: : : :		
Db	23 AGAGGGCGTTATTAACTGTC 3		
RESULT 4			
AR036420/c			
LOCUS	Sequence 12 from patent US 5872214.		
DEFINITION	22 bp DNA linear PAT 29-SEP-1999		
ACCESSION	AR036420		
VERSION	AR036420.1 GI:5953088		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 22)		
AUTHORS	Seizinger,B.R., Kley,N.A. and Bianchi,A.B.		
TITLE	NF2 isoforms		
JOURNAL	Patent: US 5872214-A 12 16-FEB-1999;		
FEATURES	Location/Qualifiers		
source	1..22		
	/organism="unknown"		

other sequences; artificial sequences.		/mol_type="unassigned DNA"	
REFERENCE	1	Query Match	57.5%; Score 13.8; DB 2; Length 22;
AUTHORS	Gunderson,K.	Best Local Similarity	70.6%; Pred. No. 5.4e+05;
TITLE	Probes and decoder oligonucleotides	Matches 12; Conservative	3; Mismatches 2; Indels 0; Gaps 0;
JOURNAL	Patent: WO 0216649-A 4341 28-FEB-2002;		
FEATURES	Illumina, Inc. (US)		
source	Location/Qualifiers		
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	/db_xref="taxon:32630"		
	/note="Computer Generated Probe Sequence."		
ORIGIN			
Query Match	65.8%; Score 15.8; DB 2; Length 25;		
Best Local Similarity	73.7%; Pred. No. 6.1e+04;		
Matches 14; Conservative	3; Mismatches 2; Indels 0; Gaps 0;		
QY	2 GAGAGGGCGUGGUUAGGC 20		
	: : : :		
Db	5 GAGAGGCGTGGTTAAGC 23		
RESULT 3			
AX538707/c			
LOCUS	Sequence 6 from Patent WO02070557.		
DEFINITION	24 bp DNA linear PAT 23-NOV-2002		
ACCESSION	AX538707		
VERSION	AX538707.1 GI:25271321		
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	other sequences; artificial sequences.		
REFERENCE	1		
AUTHORS	Fagan,R.J., Phelps,C.B., Phillips,T., Pierron,V.N., Allen,K.E., Allen,J.M. and Potter,S.J.		
TITLE	Nuclear hormone receptor ligand binding domain		
JOURNAL	Patent: WO 02070557-A 6 12-SEP-2002;		
FEATURES	Inpharmatica Limited (GB)		
source	Location/Qualifiers		
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	/note="LBDG3 Reverse primer"		
ORIGIN			
Query Match	60.8%; Score 14.6; DB 2; Length 24;		
Best Local Similarity	61.9%; Pred. No. 2.3e+05;		
Matches 13; Conservative	4; Mismatches 4; Indels 0; Gaps 0;		
QY	3 AGAGGGCGUGGUAGGCUC 23		
	: : : :		
Db	23 AGAGGGCGTTATTAACTGTC 3		
RESULT 4			
AR036420/c			
LOCUS	Sequence 12 from patent US 5872214.		
DEFINITION	22 bp DNA linear PAT 29-SEP-1999		
ACCESSION	AR036420		
VERSION	AR036420.1 GI:5953088		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 22)		
AUTHORS	Seizinger,B.R., Kley,N.A. and Bianchi,A.B.		
TITLE	NF2 isoforms		
JOURNAL	Patent: US 5872214-A 12 16-FEB-1999;		
FEATURES	Location/Qualifiers		
source	1..22		
	/organism="unknown"		

other sequences; artificial sequences.		/mol_type="unassigned DNA"	
REFERENCE	1	Query Match	57.5%; Score 13.8; DB 2; Length 22;
AUTHORS	Gunderson,K.	Best Local Similarity	70.6%; Pred. No. 5.4e+05;
TITLE	Probes and decoder oligonucleotides	Matches 12; Conservative	3; Mismatches 2; Indels 0; Gaps 0;
JOURNAL	Patent: WO 0216649-A 4341 28-FEB-2002;		
FEATURES	Illumina, Inc. (US)		
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	/note="Computer Generated Probe Sequence."		
ORIGIN			
Query Match	65.8%; Score 15.8; DB 2; Length 25;		
Best Local Similarity	73.7%; Pred. No. 6.1e+04;		
Matches 14; Conservative	3; Mismatches 2; Indels 0; Gaps 0;		
QY	2 GAGAGGGCGUGGUUAGGC 20		
	: : : :		
Db	5 GAGAGGCGTGGTTAAGC 23		
RESULT 3			
AX538707/c			
LOCUS	Sequence 6 from Patent WO02070557.		
DEFINITION	24 bp DNA linear PAT 23-NOV-2002		
ACCESSION	AX538707		
VERSION	AX538707.1 GI:25271321		
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	other sequences; artificial sequences.		
REFERENCE	1		
AUTHORS	Fagan,R.J., Phelps,C.B., Phillips,T., Pierron,V.N., Allen,K.E., Allen,J.M. and Potter,S.J.		
TITLE	Nuclear hormone receptor ligand binding domain		
JOURNAL	Patent: WO 02070557-A 6 12-SEP-2002;		
FEATURES	Inpharmatica Limited (GB)		
source	Location/Qualifiers		
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	/note="LBDG3 Reverse primer"		
ORIGIN			
Query Match	60.8%; Score 14.6; DB 2; Length 24;		
Best Local Similarity	61.9%; Pred. No. 2.3e+05;		
Matches 13; Conservative	4; Mismatches 4; Indels 0; Gaps 0;		
QY	3 AGAGGGCGUGGUAGGCUC 23		
	: : : :		
Db	23 AGAGGGCGTTATTAACTGTC 3		
RESULT 4			
AR036420/c			
LOCUS	Sequence 12 from patent US 5872214.		
DEFINITION	22 bp DNA linear PAT 29-SEP-1999		
ACCESSION	AR036420		
VERSION	AR036420.1 GI:5953088		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 22)		
AUTHORS	Seizinger,B.R., Kley,N.A. and Bianchi,A.B.		
TITLE	NF2 isoforms		
JOURNAL	Patent: US 5872214-A 12 16-FEB-1999;		
FEATURES	Location/Qualifiers		
source	1..22		
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other sequences; artificial sequences.		/mol_type="unassigned DNA"	
REFERENCE	1	Query Match	57.5%; Score 13.8; DB 2; Length 22;
AUTHORS	Gunderson,K.	Best Local Similarity	70.6%; Pred. No. 5.4e+05;
TITLE	Probes and decoder oligonucleotides	Matches 12; Conservative	3; Mismatches 2; Indels 0; Gaps 0;
JOURNAL	Patent: WO 0216649-A 4341 28-FEB-2002;		
FEATURES	Illumina, Inc. (US)		
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	/note="Computer Generated Probe Sequence."		
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Query Match	65.8%; Score 15.8; DB 2; Length 25;		
Best Local Similarity	73.7%; Pred. No. 6.1e+04;		
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QY	2 GAGAGGGCGUGGUUAGGC 20		
	: : : :		
Db	5 GAGAGGCGTGGTTAAGC 23		
RESULT 3			
AX538707/c			
LOCUS	Sequence 6 from Patent WO02070557.		
DEFINITION	24 bp DNA linear PAT 23-NOV-2002		
ACCESSION	AX538707		
VERSION	AX538707.1 GI:25271321		
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	other sequences; artificial sequences.		
REFERENCE	1		
AUTHORS	Fagan,R.J., Phelps,C.B., Phillips,T., Pierron,V.N., Allen,K.E., Allen,J.M. and Potter,S.J.		
TITLE	Nuclear hormone receptor ligand binding domain		
JOURNAL	Patent: WO 02070557-A 6 12-SEP-2002;		
FEATURES	Inpharmatica Limited (GB)		
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ORIGIN			
Query Match	60.8%; Score 14.6; DB 2; Length 24;		
Best Local Similarity	61.9%; Pred. No. 2.3e+05;		
Matches 13; Conservative	4; Mismatches 4; Indels 0; Gaps 0;		
QY	3 AGAGGGCGUGGUAGGCUC 23		
	: : : :		
Db	23 AGAGGGCGTTATTAACTGTC 3		
RESULT 4			
AR036420/c			
LOCUS	Sequence 12 from patent US 5872214.		
DEFINITION	22 bp DNA linear PAT 29-SEP-1999		
ACCESSION	AR036420		
VERSION	AR036420.1 GI:5953088		

OS	Artificial Sequence	JP 2002335977-A/34
PN	26-NOV-2002	
PD	23-AUG-2001	JP 2001252855
PF	YASUKO TERAQ, YASUSHI SHINTANI	
PI	C12N15/09, A61K45/00, A61P1/04, A61P1/10, A61P1/12, A61P1/14, A61P1/16, A61P1/18,	
PC	A61P3/10, A61P9/10, A61P9/12, A61P11/00, A61P11/06, A61P13/02,	
PC	A61P13/08, A61P15/04, A61P15/06, A61P15/08, A61P15/14, A61P25/00,	
PC	A61P25/08, A61P27/16, A61P29/00, A61P31/04, A61P37/08, A61P43/00,	
PC	C07K14/705,	
PC	C07K16/28, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12Q1/02, C12Q1/68,	
PC	G01N33/15, G01N33/50, G01N33/53, G01N33/566//A61K31/7125 PC	
PC	A61K31/713, A61K35/76,	
PC	A61K48/00, C12N15/00, C12N5/00	
CC	Novel G protein coupled receptor protein and its DNA FH	Key
FT	source	1..28
FT	Location/Qualifiers	/organism='Artificial Sequence'
FEATURES	source	1..28
	Location/Qualifiers	/organism='synthetic construct'
	/mol_type='genomic DNA'	
	/db_xref='taxon:32630'	
ORIGIN		
Query Match	55.8%;	Score 13.4; DB 2; Length 28;
Best Local Similarity	60.9%;	Pred. No. 7.9e+05;
Matches	14; Conservative	3; Mismatches 6; Indels 0; Gaps 0;
QY	1	UCGAGGGGCGUUAAGCGCUC 23
Db	6	TGAGAGGTGCTGTGCAAGTCTTC 28
RESULT 9		
LOCUS	AR148541/c	25 bp DNA linear PAT 08-AUG-2001
DEFINITION	Sequence 23 from patent US 6225115.	
ACCESSION	AR148541	
VERSION	AR148541.1	GI:15112631
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 25)	
AUTHORS	Smith, K.E., Borden, L.A., Weinhank, R.L. and Hartig, P.R.	
TITLE	DNA encoding taurine and GABA transporters and uses thereof	
JOURNAL	Patent: US 6225115-A 23 01-MAY-2001;	
FEATURES	Location/Qualifiers	
source	1..25	
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	/mol_type='unassigned DNA'	
ORIGIN		
Query Match	55.0%;	Score 13.2; DB 2; Length 25;
Best Local Similarity	66.7%;	Pred. No. 1e+06;
Matches	12; Conservative	3; Mismatches 3; Indels 0; Gaps 0;
QY	5	AGGGGCGUUAAGCGCU 22
Db	23	AGGTGCTGTGTAAGGCAT 6
RESULT 10		
LOCUS	I62320/c	25 bp DNA linear PAT 07-OCT-1997
DEFINITION	Sequence 23 from patent US 5658786.	
ACCESSION	I62320	

VERSION I62320.1 GI:2480268
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Smith,K.E., Weinschank,R.L., Borden,L.A. and Hartig,P.R.
TITLE DNA encoding rat taurine transporter and uses thereof
JOURNAL Patent: US 5658786-A 23 19-AUG-1997;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 55.0%; Score 13.2; DB 2; Length 25;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 5 AGGGGCGGUGUAGGCGU 22
Db 23 AGGTGCTGGTGAAGGCAT 6
RESULT 11
AX215297/c
LOCUS AX215297 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 739 from Patent WO0159103.
ACCESSION AX215297
VERSION AX215297.1 GI:15525340
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
Patent: WO 0159103-A 739 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
ORIGIN
Query Match 54.2%; Score 13; DB 2; Length 17;
Best Local Similarity 84.6%; Pred. No. 1.4e+06;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 UGAGAGGGGCGUG 13
Db 16 TGAGAGGGGCTGG 4
RESULT 12
AX215298/c
LOCUS AX215298 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 740 from Patent WO0159103.
ACCESSION AX215298
VERSION AX215298.1 GI:15525341
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
Patent: WO 0159103-A 740 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)

RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
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Query Match 54.2%; Score 13; DB 2; Length 17;
Best Local Similarity 84.6%; Pred. No. 1.4e+06;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 UGAGAGGGGCGUG 13
Db 15 TGAGAGGGGCTGG 3
RESULT 13
AX215299/c
LOCUS AX215299 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 741 from Patent WO0159103.
ACCESSION AX215299
VERSION AX215299.1 GI:15525342
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
Patent: WO 0159103-A 741 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
ORIGIN
Query Match 54.2%; Score 13; DB 2; Length 17;
Best Local Similarity 84.6%; Pred. No. 1.4e+06;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 UGAGAGGGGCGUG 13
Db 14 TGAGAGGGGCTGG 2
RESULT 14
AX215300/c
LOCUS AX215300 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 742 from Patent WO0159103.
ACCESSION AX215300
VERSION AX215300.1 GI:15525343
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
Patent: WO 0159103-A 742 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"

/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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ORIGIN

Query Match 54.2%; Score 13; DB 2; Length 17;
Best Local Similarity 84.6%; Pred. No. 1.4e+06;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGAGAGGGCGCUGG 13
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Db 13 TGAGAGGGGCTGG 1

RESULT 15

AX298773/c
LOCUS AX298773 20 bp DNA linear PAT 26-NOV-2001
DEFINITION Sequence 407 from Patent WO0183749.

ACCESSION AX298773

VERSION AX298773.1 GI:17128763

KEYWORDS

SOURCE Mus sp.

ORGANISM Mus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 Bachmanov, A.A., Beauchamp, G.K., Chatterjee, A., de Jong, P.J., Li, S.,

Li, X., Ohmen, J.D., Reed, D.R., Ross, D. and Tordoff, M.G.

Gene and sequence variation associated with sensing carbohydrate

compounds and other sweeteners

Patent: WO 0183749-A 407 08-NOV-2001;

WARNER-LAMBERT COMPANY (US) ; The Monell Chemical Senses Center

(US)

FEATURES

source

1..20

/organism="Mus sp."

/mol_type="unassigned DNA"

/db_xref="taxon:10095"

ORIGIN

Query Match 54.2%; Score 13; DB 2; Length 20;
Best Local Similarity 84.6%; Pred. No. 1.3e+06;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGAGAGGGCGCUGG 13
:|||||:|||||
Db 19 TGAGAGGGGCTGG 7

Search completed: October 16, 2006, 14:52:12

Job time : 591.797 secs

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GenCore version 5.1.9

Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:04:23 ; Search time 1032.18 Seconds
(without alignments)
1300.222 Million cell updates/sec

Title: US-10-604-726A-6034

Perfect score: 24

Sequence: 1 ugagagggcgguuagcgucc 24

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 56556

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13.4	55.8	27	14	AJ591134 Arabidops
C 2	12.6	52.5	24	11	AZ806300 2M0068F13
C 3	12.2	50.8	28	13	CZ443094 IBBD03.f
C 4	12	50.0	22	1	AI473941 tm04c11.x
C 5	12	50.0	25	10	R99803 vp91b12.r1
C 6	11.8	49.2	27	14	AG613296 Escherich
C 7	11.8	49.2	28	14	ATH531105 Arabidops
C 8	11.8	49.2	29	11	AZ346559 1M0081M15
C 9	11.6	48.3	21	11	AZ654730 1M0529P05
C 10	11.6	48.3	27	11	AZ970595 2M0243T18
C 11	11.6	48.3	27	12	CG712990 1119029H1
C 12	11.6	48.3	27	12	CG725093 1119083H1
C 13	11.6	48.3	30	14	AB081884 Drosophila
C 14	11.4	47.5	25	11	AZ794596 Arabidops
C 15	11.4	47.5	30	11	AZ375590 1M0129H06
C 16	11.2	46.7	24	11	AZ341038 1M0073B16
C 17	11.2	46.7	25	11	AZ820085 2M0092001
C 18	11.2	46.7	27	14	AJ591135 Arabidops
C 19	11	45.8	20	11	AZ846437 2M0146E10

20	11	45.8	21	11	AZ493166
C 21	11	45.8	21	11	AZ836049
22	11	45.8	21	11	AZ945526
23	11	45.8	27	11	AZ948983
24	11	45.8	28	11	AZ441037
25	11	45.8	28	11	AZ802448
C 26	11	45.8	28	12	CG725337
C 27	11	45.8	29	13	CZ443020
C 28	11	45.8	30	11	AZ976285
C 29	10.8	45.0	22	1	AI183338
C 30	10.6	44.2	27	14	TA385H06Q
C 31	10.6	44.2	20	11	AZ346729
C 32	10.6	44.2	25	11	AZ851549
C 33	10.6	44.2	26	11	AZ786348
C 34	10.6	44.2	26	12	CG729580
C 35	10.6	44.2	28	11	AZ591936
C 36	10.6	44.2	28	13	CZ472926
C 37	10.6	44.2	29	11	AZ406476
C 38	10.6	44.2	30	11	AZ460736
C 39	10.6	44.2	30	12	CG717040
C 40	10.6	44.2	30	13	CZ473194
C 41	10.4	43.3	19	11	AZ595016
C 42	10.4	43.3	22	1	AA978171
C 43	10.4	43.3	24	11	AZ786207
C 44	10.4	43.3	26	13	CM020366
C 45	10.4	43.3	28	11	AZ665590

ALIGNMENTS

RESULT 1	AJ591134/c	27 bp	DNA	linear	GSS 15-JAN-2004
LOCUS	Arabidopsis thaliana T-DNA flanking sequence, left border, clone				
DEFINITION	580805 genomic survey sequence.				
ACCESSION	AJ591134				
VERSION	AJ591134.1	GI:37940758			
KEYWORDS	GSS; left border; T-DNA flanking sequence.				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
REFERENCE	1				
AUTHORS	Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Sanson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M., and Lecharny, A.				
TITLE	T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites				
JOURNAL	EMBO Rep. 3 (12), 1152-1157 (2002)				
PUBMED	12446565				
REFERENCE	2 (bases 1 to 27)				
AUTHORS	Balzergue, S.				
TITLE	Direct Submission				
JOURNAL	Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE				
COMMENT	PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbgap.versailles.inra.fr/publiclines/ . This sequence has been generated in the framework of the French plant genomics program 'genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).				
FEATURES	Location/Qualifiers				
source	1..27				
	/organism="Arabidopsis thaliana"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:3702"				

misc_feature 1..27 /clone_lib="Arabidopsis thaliana T-DNA insertion lines" /ecotype="Waasilewskija" /notes="T-DNA flanking sequence left border"

ORIGIN

Query Match 55.8%; Score 13.4; DB 14; Length 27;
Best Local Similarity 73.3%; Pred. No. 3.1e+05;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGGGGCGUGGUUAAAGG 19
|||||:|:|:|:|
Db 21 AGGGGCTGGTTACG 7

RESULT 2
AZ806300 24 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0068F13F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
DEFINITION clone UUGC2M0068F13 F, genomic survey sequence.

ACCESSION AZ806300
VERSION AZ806300.1 GI:12967111
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Islan,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., fingsy,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0068 row: F column: 13
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0068F13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 52.5%; Score 12.6; DB 11; Length 24;
Best Local Similarity 57.9%; Pred. No. 6.9e+05;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 UGAGAGGGCGUGGUUAAAGG 19
:|||||:|:|:|:|
Db 5 TGGGAGTGGTGGTTAGG 23

RESULT 3
CZ443094/c 28 bp DNA linear GSS 07-APR-2005
LOCUS IB8BD03.fwd HIV-vector integration sites from well-expressed
DEFINITION proviruses in human Jurkat T cells Homo sapiens genomic clone
IB8BD03.fwd, genomic survey sequence.

ACCESSION CZ443094
VERSION CZ443094.1 GI:62379366
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 28)
Lewinski,M.K., Bisgrove,D., Shinn,P., Chen,H., Hoffmann,C., Hannehalli,S., Verdin,E., Berry,C.C., Eckert,J.R. and Bushman,F.D.
TITLE Genome-wide analysis of chromosomal features repressing human immunodeficiency virus transcription
J. Virol. 79 (11), 6610-6619 (2005)
15890899
COMMENT Contact: Bushman FD
Department of Microbiology
University of Pennsylvania School of Medicine
402C Johnson Pavilion, 3610 Hamilton Walk, Philadelphia, PA 19104-6076, USA
Tel: 215 573 8732
Fax: 215 573 4856
Email: bushman@mail.med.upenn.edu
Class: PCR with specific primers.
Location/Qualifiers
1..28
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="IB8BD03.fwd"
/cell_line="Jurkat"
/clone_lib="HIV-vector integration sites from well-expressed proviruses in human Jurkat T cells"
/note="Vector: LTR-Tat-IRES-GFP (pEV731); We have investigated regulatory sequences in noncoding human DNA that are associated with repression of an integrated human immunodeficiency virus type 1 (HIV-1) promoter. HIV-1 integration results in the formation of precise and homogeneous junctions between viral and host DNA, but integration takes place at many locations. Thus, the variation in HIV-1 gene expression at different integration sites reports the activity of regulatory sequences at nearby chromosomal positions. Negative regulation of HIV transcription is of particular interest because of its association with maintaining HIV in a latent state in cells from infected patients. To identify chromosomal regulators of HIV transcription, we infected Jurkat T cells with an HIV-based vector transducing green fluorescent protein (GFP) and separated cells into

populations containing well-expressed (GFP-positive) or poorly expressed (GFP-negative) proviruses. We then determined the chromosomal locations of the two classes by sequencing 971 junctions between viral and cellular DNA. Possible effects of endogenous cellular transcription were characterized by transcriptional profiling. Low-level GFP expression correlated with integration in (i) gene deserts, (ii) centromeric heterochromatin, and (iii) very highly expressed cellular genes. These data provide a genome-wide picture of chromosomal features that repress transcription and suggest models for transcriptional latency in cells from HIV-infected patients."

ORIGIN

Query Match 50.0%; Score 12.2; DB 13; Length 28;
Best Local Similarity 64.7%; Pred. No. 1.1e+06;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGAGGGGCGUUAAGC 19
|||||||:|:|
Db 20 AGAGGGGCGCTTGGGG 4

RESULT 4

AI473941/c 22 bp mRNA linear EST 09-MAR-1999
LOCUS tm04c11.x1 NCI CGAP Col4 Homo sapiens cDNA clone IMAGE:2155604 3'
DEFINITION similar to TR:Q06459 Q06459 NUCLEOLIN.; mRNA sequence.

ACCESSION AI473941
VERSION AI473941
KEYWORDS EST.
SOURCE AI473941.1 GI:4326986

ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo

1 (bases 1 to 22)

REFERENCE

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

FEATURES

source

1..22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2155604"
/tissue_type="moderately-differentiated adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Col4"
/note="Organ: Colon; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.7 Kb. Life Technologies catalog #: 11531-019"

ORIGIN

Query Match 50.0%; Score 12; DB 1; Length 22;
Best Local Similarity 70.0%; Pred. No. 1.3e+06;
Matches 14; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY

2 GAGAGGGGCGUUAAGCG 21
|||||||:|:|

Db

20 GAGAGGGGCGGTCGAGGG 1

RESULT 5

R89803/c

LOCUS

DEFINITION

(HUMAN); mRNA sequence.

ACCESSION

R89803

VERSION

R89803.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo

1 (bases 1 to 25)

REFERENCE

AUTHORS

Willson, R.

THE WASHU-MERCK EST PROJECT

UNPUBLISHED (1995)

CONTACT: WILSON RK

WASHINGTON UNIVERSITY SCHOOL OF MEDICINE

4444 FOREST PARK PARKWAY, BOX 8501, ST. LOUIS, MO 63108

TEL: 314 286 1800

FAX: 314 286 1810

EMAIL: est@watson.wustl.edu

INSERT SIZE: 1193

HIGH QUALITY SEQUENCE STARTS: 1

HIGH QUALITY SEQUENCE STOPS: 1

SOURCE: IMAGE Consortium, LLNL

THIS CLONE IS AVAILABLE ROYALTY-FREE THROUGH LLNL; CONTACT THE

IMAGE Consortium (info@image.llnl.gov) FOR FURTHER INFORMATION.

TRACE CONSIDERED OVERALL POOR QUALITY

INSERT LENGTH: 1193

STD ERROR: 0.00

SEQ PRIMER: M13RFL

HIGH QUALITY SEQUENCE STOP: 1.

LOCATION/QUALIFIERS

1..25

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3763833"

/db_xref="taxon:9606"

/clone="IMAGE:194783"

/sex="male"

/dev_stage="20 week-post conception fetus"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares fetal liver spleen INFLS"

/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)

with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;

1st strand cDNA was primed with a Pac I - oligo(dT) primer

[5' AACTGGAAGAATTAATTAAGATCTTTTTTTTTTTTTTTT 3']

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Pac I and cloned into the Pac I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M.Fatima Bonaldo."

Query Match 50.0%; Score 12; DB 10; Length 25;

Best Local Similarity 75.0%; Pred. No. 1.3e+06;

Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGGCGUUA 17

|||||||:|:|

Db 12 GGGGCTGGTTAA 1

```

RESULT 6
AG613296/c
LOCUS
DEFINITION
  Escherichia coli K12 MG1655 DNA, clone: 431F, genomic survey
  sequence.
ACCESSION
  AG613296
VERSION
  AG613296.1 GI:41224745
KEYWORDS
  GSS.
SOURCE
  Escherichia coli K12
ORGANISM
  Escherichia coli K12
  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Enterobacteriaceae; Escherichia.
REFERENCE
  1 Hayaashi,K., Morooka,N., Mori,H. and Horiuchi,T.
  A more accurate sequence comparison between genomes of Escherichia
  coli K12 W3110 and MG1655 strains
  Unpublished
JOURNAL
  2 (bases 1 to 27)
  Hayaashi,K., Morooka,N. and Horiuchi,T.
  Direct Submission
  Submitted (19-JAN-2004) Takashi Horiuchi, National Institute for
  Basic Biology, Gene Expression and Regulation II, 38 Nishigo-naka,
  Myodaiji-cho, Okazaki, Aichi 444-8595, Japan
  (E-mail:kishori@nibb.ac.jp, Tel:81-564-55-7690, Fax:81-564-55-7695)
  Location/Qualifiers
FEATURES
  source
    1..27
    /organism="Escherichia coli K12"
    /mol_type="genomic DNA"
    /strain="K12"
    /sub_strain="MG1655"
    /db_xrefs="taxon:83333"
    /clone="431F"
    /notes="The 5' end of this sequence corresponds to 9729(c)
    of Acc#: AE000431.
    This is located within REP element."
ORIGIN
  Query Match 49.2%; Score 11.8; DB 14; Length 27;
  Best Local Similarity 73.3%; Pred. No. 1.6e+06;
  Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
  QY 8 GGCUGGUUAGGCGU 22
  ||| ||| ||| ||| ||| |||
  Db 23 GCGCGGATAGGCGT 9
  ||| ||| ||| ||| ||| |||

RESULT 7
ATH531105
LOCUS
DEFINITION
  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
  225H06, genomic survey sequence.
ACCESSION
  AJ531105
VERSION
  AJ531105.1 GI:26799365
KEYWORDS
  GSS; left border; T-DNA flanking sequence.
SOURCE
  Arabidopsis thaliana (thale cress)
ORGANISM
  Arabidopsis thaliana
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
  1 Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
  Chauvin,S., Bechtold,N., Cruaud,C., Dekosse,R., Pelletier,G.,
  Lepiniec,L., Caboche,M. and Lecharny,A.
  T-DNA integration into the Arabidopsis genome depends on sequences
  of pre-insertion sites
  EMBO Rep. 3 (12), 1152-1157 (2002)
JOURNAL
  PUBMED
  12446565
  2 (bases 1 to 28)
  Balzergue,S.
  Direct Submission
  Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
  Gaston Cremieux, 91057 Evry cedex, FRANCE
  PCR was performed on DNA from transformants of Arabidopsis thaliana
  plants from INRA (Versailles). The DNA fragment(s) resulting from
  the PCR were directly sequenced from the left or the right border
  to determine the genomic sequence flanking the insertion. T-DNA
  derived sequences were removed. Information to order the
  corresponding mutant line and a link to a database providing a
  graphical display of the insertion site are available at
  http://dbgap.versailles.inra.fr/publiclines/. This sequence has
  been generated in the framework of the French plant genomics
  program 'Genoplatte' (http://www.genoplatte.com and
  http://genoplatte-info.infobiogen.fr).
  Location/Qualifiers
FEATURES
  source
    1..28
    /organism="Arabidopsis thaliana"
    /mol_type="genomic DNA"
    /cultivar="Wassilewskija"
    /db_xref="taxon:3702"
    /clone="225H06"
    /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
    /ecotype="Wassilewskija"
    /note="T-DNA flanking sequence
    left border"
  misc_feature
    1..28
    /note="T-DNA flanking sequence
    left border"
ORIGIN
  Query Match 49.2%; Score 11.8; DB 14; Length 28;
  Best Local Similarity 60.9%; Pred. No. 1.6e+06;
  Matches 14; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
  QY 2 GAGAGGGCGUGGUUAGGCGUCC 24
  ||||| ||| ||| ||| ||| |||
  Db 3 GAGAGGGCGGTATATGATGTC 25
  ||||| ||| ||| ||| ||| |||

RESULT 8
AZ346559
LOCUS
DEFINITION
  1M0081M15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0081M15 R, genomic survey sequence.
ACCESSION
  AZ346559
VERSION
  AZ346559.1 GI:10425796
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 29)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunne@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0081 row: M column: 15
  Seq primer: CACACAGGAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 29.
  Location/Qualifiers
FEATURES
  source
    1..29
    /organism="Mus musculus"
    /mol_type="genomic DNA"

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0529P05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

ORIGIN

```

Query Match      49.2%; Score 11.8; DB 11; Length 29;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY 4 GAGGGCGUGGUAAAG 18
    |||||:::|||||
Db 6 GAAGGTCGTGTTAAG 20

```

RESULT 9

```

AZ654730/c
LOCUS          21 bp      DNA      linear      GSS 14-DEC-2000
DEFINITION    1M0529P05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0529P05 F, genomic survey sequence.
ACCESSION     AZ654730
VERSION       AZ654730.1 GI:11791876
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 21)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
JOURNAL       Contact: Robert B. Weiss
COMMENT       University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0529 row: P column: 05
              Seq primer: CGTTGTAACGACGCCAGT
              Class: plasmid ends
              High quality sequence stop: 21.
FEATURES      Location/Qualifiers
               1..21
               /organism="Mus musculus"

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0529P05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

ORIGIN

```

Query Match      48.3%; Score 11.6; DB 11; Length 21;
Best Local Similarity 66.7%; Pred. No. 1.9e+06;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 2 GAGAGGGCGUGGUAAAG 19
    |||||:::|||||
Db 19 GGGTGGGATGGGTAAG 2

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RESULT 10

```

AZ970595
LOCUS          27 bp      DNA      linear      GSS 27-APR-2001
DEFINITION    2M0243118R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0243118 R, genomic survey sequence.
ACCESSION     AZ970595
VERSION       AZ970595.1 GI:13841822
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 27)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
JOURNAL       Contact: Robert B. Weiss
COMMENT       University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0243 row: I column: 18
              Seq primer: CACAGAGAAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 27.
FEATURES      Location/Qualifiers
               1..27

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0243118"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

ORIGIN

```

Query Match      48.3%; Score 11.6; DB 11; Length 27;
Best Local Similarity 61.1%; Pred. No. 1.9e+06;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      2 GAGAGGGCGUGUUAAGG 19
      |||||:::||:|
Db      1 GCGAGTGGGCGTTAGG 18

```

RESULT 11

```

CG712990/c
LOCUS      27 bp      DNA      linear      GSS 20-OCT-2003
DEFINITION      1119029H12.2EL.Y1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.
ACCESSION      CG712990
VERSION      CG712990.1 GI:37738896
KEYWORDS      GSS.
SOURCE      Zea mays
ORGANISM      Zea mays

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 27)

```

REFERENCE

```

AUTHORS      Walbot,V.
TITLE      Maize genomic sequences found using engineered RescueMu transposon
JOURNAL      Unpublished (2001)
COMMENT      Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119029 row: H column: 12
Class: transposon-tagged.
Location/Qualifiers
1..27
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:10090"
/tissue_type="leaf"

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FEATURES

Source

```

/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:10090"
/tissue_type="leaf"

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/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

```

ORIGIN

```

Query Match      48.3%; Score 11.6; DB 12; Length 27;
Best Local Similarity 61.1%; Pred. No. 1.9e+06;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      4 GAGGGCGUGUUAAGCG 21
      |||||:::||:|
Db      18 GATGAGCTGTTATGCG 1

```

RESULT 12

```

CG725093/c
LOCUS      27 bp      DNA      linear      GSS 20-OCT-2003
DEFINITION      1119083H11.2EL.Y1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.
ACCESSION      CG725093
VERSION      CG725093.1 GI:37762551
KEYWORDS      GSS.
SOURCE      Zea mays
ORGANISM      Zea mays

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 27)

```

REFERENCE

```

AUTHORS      Walbot,V.
TITLE      Maize genomic sequences found using engineered RescueMu transposon
JOURNAL      Unpublished (2001)
COMMENT      Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119083 row: H column: 11
Class: transposon-tagged.
Location/Qualifiers
1..27
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using

```

FEATURES

Source

```

/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"

```

BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 48.3%; Score 11.6; DB 12; Length 27;
Best Local Similarity 61.1%; Pred. No. 1.9e+06;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 GAGGGGCGUGUUAAGCGC 21
|||||:|||||

Db 18 GATGAGCTGTTATGGCG 1
|||||:|||||

RESULT 13

AB081884

LOCUS

DEFINITION Drosophila melanogaster DNA, clone:1(2)SH2 0127, genomic survey

sequence.

AB081884

VERSION AB081884.1

KEYWORDS GI:21623894

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1

AUTHORS Oh, S. W., Kingsley, T., Shin, H. H., Zheng, Z., Chen, H. W., Chen, X.,

Wang, H., Ruan, P., Moody, M. and Hou, S. X.

TITLE A p-element insertion screen identified mutations in 455 novel

essential genes in Drosophila

Genetics 163 (1), 195-201 (2003)

PUBMED 12586707

REFERENCE 2 (bases 1 to 30)

AUTHORS Oh, S., Kingsley, T., Shin, H., Zheng, Z., Chen, H. and Hou, S.

TITLE Direct Submission

JOURNAL Submitted (21-MAR-2002) Suwan Oh, The Laboratory of Immunobiology,

National Institutes of Health, National Cancer Institute,

Frederick; 1050 Boyles st., Frederick, Maryland 21702-1201, USA

(E-mail:chuwan@mail.ncifcrf.gov, Tel:1-301-846-7314,

Fax:1-301-846-6145)

FEATURES

source

1..30

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone="1(2)SH2 0127"

ORIGIN

Query Match 48.3%; Score 11.6; DB 14; Length 30;

Best Local Similarity 61.1%; Pred. No. 2e+06;

Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 GGGGCGUGUUAAGCGCUC 23
|||||:|||||

Db 6 GGGTCTTATAAGCGCTC 23
|||||:|||||

RESULT 14

AZ794596

LOCUS

DEFINITION 2M0048M20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0048M20 F, genomic survey sequence.

ACCESSION AZ794596

VERSION AZ794596.1

KEYWORDS GI:12940723

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 25)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D. Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0048 row: M column: 20

Seq primer: CGTTGTAACACGAGCGCCAGT

Class: plasmid ends

High quality sequence stop: 25.

FEATURES

source

1..25

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0048M20"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: FWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

ligonucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (GI|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 47.5%; Score 11.4; DB 11; Length 25;

Best Local Similarity 57.1%; Pred. No. 2.4e+06;

Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 UGAGAGGGCGUGUUAAGCGC 21
:|||||:|||||

Db 5 TGGGAGGGGGTGTGAGGGG 25
:|||||:|||||

RESULT 15

AZ375590/c

LOCUS

DEFINITION 1M0129H06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0129H06 F, genomic survey sequence.

ACCESSION AZ375590

VERSION AZ375590.1

KEYWORDS GI:10489290

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 30)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islan,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0129 row: H column: 06
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 30.
FEATURES
source
1..30
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0129H06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 47.5%; Score 11.4; DB 11; Length 30;
Best Local Similarity 52.4%; Pred. No. 2.4e+06;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 UGAGAGGGCGGCUUAAAGCG 21
:|||||:|||||
DB 27 TGAAGAAGGAGTTGTTAAGGG 7

Search completed: October 16, 2006, 15:51:23
Job time : 1034.18 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:11:03 ; Search time 55.5789 Seconds
(without alignments)
807.979 Million cell updates/sec

Title: US-10-604-726A-6034

Perfect score: 24

Sequence: 1 ugagagggcgguuaagggucc 24

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 1097684

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1 COMB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5 COMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B COMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H COMB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PC/US COMB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.2	63.3	28	3	US-08-814-052-53
C 2	14	58.3	25	3	US-09-396-1960-15707
C 3	13.8	57.5	22	2	US-08-179-738-12
C 4	13.8	57.5	22	2	US-08-828-145-12
C 5	13.2	55.0	25	2	US-08-295-814E-23
C 6	13.2	55.0	25	3	US-09-343-361-23
C 7	13	54.2	27	4	US-09-598-982C-7
C 8	12.8	53.3	19	2	US-08-460-751-27
C 9	12.8	53.3	25	3	US-09-641-259B-31
C 10	12.6	52.5	19	3	US-10-059-579A-123
C 11	12.6	52.5	20	3	US-09-166-186-119
C 12	12.6	52.5	20	3	US-09-313-932-119
C 13	12.6	52.5	20	3	US-09-580-052-51
C 14	12.6	52.5	21	3	US-08-520-373D-31
C 15	12.6	52.5	25	3	US-09-443-067-45
C 16	12.6	52.5	25	3	US-09-396-1960-3644
C 17	12.6	52.5	25	3	US-09-396-1960-29254
C 18	12.6	52.5	28	3	US-09-529-239D-21
C 19	12.6	52.5	30	3	US-08-840-316-65
C 20	12.6	52.5	30	3	US-08-840-316-102
C 21	12.6	52.5	30	3	US-08-809-523-65
C 22	12.6	52.5	30	3	US-08-809-523-102
C 23	12.6	52.5	30	3	US-08-471-971-65

C 24	12.6	52.5	30	3	US-08-471-971-102	Sequence 102, Appl
C 25	12.6	52.5	30	3	US-09-402-776-65	Sequence 65, Appl
C 26	12.6	52.5	30	3	US-09-402-776-102	Sequence 102, Appl
C 27	12.6	52.5	30	3	US-09-291-129-10	Sequence 10, Appl
C 28	12.6	52.5	30	3	US-08-470-246-65	Sequence 65, Appl
C 29	12.6	52.5	30	3	US-08-470-246-102	Sequence 102, Appl
C 30	12.6	52.5	30	3	US-08-316-765-65	Sequence 65, Appl
C 31	12.6	52.5	30	3	US-08-316-765-102	Sequence 102, Appl
C 32	12.6	52.5	30	3	US-09-724-475-102	Sequence 65, Appl
C 33	12.6	52.5	30	3	US-09-724-475-102	Sequence 102, Appl
C 34	12.6	52.5	30	7	PCT-US93-08849A-65	Sequence 65, Appl
C 35	12.6	52.5	30	7	PCT-US93-08849A-65	Sequence 65, Appl
C 36	12.4	51.7	24	3	US-09-630-377-11	Sequence 11, Appl
C 37	12.4	51.7	25	3	US-09-396-196G-41852	Sequence 41852, A
C 38	12.4	51.7	25	3	US-09-396-196G-58488	Sequence 58488, A
C 39	12.4	51.7	25	3	US-09-396-196G-73489	Sequence 73489, A
C 40	12.4	51.7	25	3	US-09-396-196G-78586	Sequence 78586, A
C 41	12.4	51.7	25	3	US-09-396-196G-122139	Sequence 122139, A
C 42	12.4	51.7	25	3	US-09-396-196G-122140	Sequence 122140, A
C 43	12.2	50.8	19	3	US-09-422-978-9132	Sequence 9132, Ap
C 44	12.2	50.8	20	2	US-08-117-952-440	Sequence 440, Appl
C 45	12.2	50.8	20	3	US-09-526-193A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-814-052-53/c
; Sequence 53, Application US/08814052
; Patent No. 6015783
; GENERAL INFORMATION:
; APPLICANT: von der Osten, Claus
; APPLICANT: Cherry, Joel R.
; APPLICANT: Bjornvad, Mads E.
; APPLICANT: Vind, Jesper
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: PROCESS FOR REMOVAL OR BLEACHING OF SOILING
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSER: No. 6015783o No. 6015783disk of No. 6015783th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,052
; FILING DATE: 06-MAR-1997
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4684.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-814-052-53

Query Match 63.3%; Score 15.2; DB 3; Length 28;

Best Local Similarity 75.0%; Pred. No. 5.5e+02;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAGGGGCGGUUAAGGCG 21
Db 20 GCGAGTGGCTGGTCAAGGCG 1

RESULT 2

US-09-396-196G-15707/c
; Sequence 15707, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Wittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15707
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-15707

Query Match 58.3%; Score 14; DB 3; Length 25;
Best Local Similarity 54.5%; Pred. No. 2e+03;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 UGAGAGGGGCGGUUAAGGCGU 22
Db 22 TGAGATGAGCTGCTTAACGAGT 1

RESULT 3

US-08-179-738-12/c
; Sequence 12, Application US/08179738
; Patent No. 5578462
; GENERAL INFORMATION:
; APPLICANT: Seizinger, Bernd R.
; APPLICANT: Kley, Nikolai A.
; APPLICANT: Bianchi, Albert B.
; TITLE OF INVENTION: No. 5578462e1 NF2 Isoforms
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: U.S.A
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/179,738
; FILING DATE: 10-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Robins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5998-0017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231

; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-179-738-12

Query Match 57.5%; Score 13.8; DB 2; Length 22;
Best Local Similarity 70.6%; Pred. No. 2.5e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGAGGGGCGGUUAAGG 19
Db 17 AGAGGAGCTGGTTCAGG 1

RESULT 4

US-08-628-145-12/c
; Sequence 12, Application US/08628145
; Patent No. 5872214
; GENERAL INFORMATION:
; APPLICANT: Seizinger, Bernd R.
; APPLICANT: Kley, Nikolai A.
; APPLICANT: Bianchi, Albert B.
; TITLE OF INVENTION: No. 5872214e1 NF2 Isoforms
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: U.S.A
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,145
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/179,738
; FILING DATE: 10-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Robins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5998-0017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-628-145-12

Query Match 57.5%; Score 13.8; DB 2; Length 22;
Best Local Similarity 70.6%; Pred. No. 2.5e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGAGGGGCGGUUAAGG 19
Db 17 AGAGGAGCTGGTTCAGG 1

RESULT 5

US-08-295-814E-23/c
; Sequence 23, Application US/08295814E
; Patent No. 5658786
; GENERAL INFORMATION:
; APPLICANT: Smith, Kelli E.
; APPLICANT: Borden, Laurence A.
; APPLICANT: Hartig, Paul R.
; APPLICANT: Weinschenk, Richard L.
; TITLE OF INVENTION: DNA ENCODING TAURINE AND GABA
; TITLE OF INVENTION: TRANSPORTERS AND USES THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,814E
; FILING DATE: DECEMBER 19, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40558-B-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-295-814E-23

Query Match 55.0%; Score 13.2; DB 2; Length 25;
Best Local Similarity 66.7%; Pred. No. 4.9e+03;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 5 AGGGCGUGGUUAGGCGU 22
Db 23 AGGTGCTGTGAGGCAT 6

RESULT 6
US-09-343-361-23/c
; Sequence 23, Application US/09343361
; Patent No. 6225115
; GENERAL INFORMATION:
; APPLICANT: Smith, Kelli E. et al
; TITLE OF INVENTION: DNA Encoding Taurine and GABA Transporters and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 40558-D
; CURRENT APPLICATION NUMBER: US/09/343,361
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 23
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-343-361-23

Query Match 55.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 66.7%; Pred. No. 4.9e+03;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 5 AGGGCGUGGUUAGGCGU 22
Db 23 AGGTGCTGTGAGGCAT 6

RESULT 7
US-09-598-982C-7
; Sequence 7, Application US/09598982C
; Patent No. 6936260
; GENERAL INFORMATION:
; APPLICANT: Niles, Andrew
; APPLICANT: Maflitt, Mark
; APPLICANT: Haak-Frendscho, Mary
; TITLE OF INVENTION: RECOMBINANT PROTEOLYTIC TRYPTASES, ACTIVE SITE MUTANTS THEREOF,
; TITLE OF INVENTION: AND METHODS OF MAKING SAME
; FILE REFERENCE: 34506.104
; CURRENT APPLICATION NUMBER: US/09/598,982C
; CURRENT FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 09/079,970
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutagenesis oligonucleotide
US-09-598-982C-7

Query Match 54.2%; Score 13; DB 4; Length 27;
Best Local Similarity 66.7%; Pred. No. 6.2e+03;
Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 4 GAGGGCGUGGUUAGGCGUCC 24
Db 1 GAGGAGCCGCTGAGGCTCTCC 21

RESULT 8
US-08-460-751-27
; Sequence 27, Application US/08460751
; Patent No. 5891628
; GENERAL INFORMATION:
; APPLICANT: Reeders, Stephen
; APPLICANT: Schneider, Michael
; APPLICANT: Glucksmann, Sandra
; TITLE OF INVENTION: IDENTIFICATION OF POLYCYSTIC KIDNEY
; TITLE OF INVENTION: DISEASE GENE, DIAGNOSTICS AND TREATMENT
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,751
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; OTHER INFORMATION: Description of Artificial Sequence: primer
; APPLICATION NUMBER: US 08/413,580
; FILING DATE: 03-MAR-1995

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; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7638-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-460-751-27

Query Match 53.3%; Score 12.8; DB 2; Length 19;
Best Local Similarity 62.5%; Pred. No. 7.3e+03;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCUGGUUAGGCGUCC 24
Db 1 GCTCTTTAAGCGCTCC 16

RESULT 9
US-09-641-259B-31/c
; Sequence 31, Application US/09641259B
; Patent No. 6468756
; GENERAL INFORMATION:
; APPLICANT: Bonini, James A
; APPLICANT: Borowsky, Beth E
; APPLICANT: Adam, Nika
; APPLICANT: Boyle, No. 64687561
; APPLICANT: Thompson, Thelma O.
; TITLE OF INVENTION: DNA Encoding SNORF25 Receptor
; FILE REFERENCE: 1795/56095-B/JPM/ADM
; CURRENT APPLICATION NUMBER: US/09/641,259B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: PCT/US00/04413
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 09/387,699
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: US 09/255,376
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer/ Probe
US-09-641-259B-31

Query Match 53.3%; Score 12.8; DB 3; Length 25;
Best Local Similarity 68.8%; Pred. No. 7.6e+03;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGGGCGUGGUUAGG 19
Db 20 GAGGGCGTCTTAATG 5

RESULT 10
US-10-059-579A-123/c
; Sequence 123, Application US/10059579A
; Patent No. 6835541
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: SUKUMAR, Saraswati
; APPLICANT: EVRON, Ella

; ATTORNEY/AGENT INFORMATION:
; NAME: DOOLEY, William C.
; APPLICANT: DAVIDSON, Nancy
; APPLICANT: FACKLER, Mary Jo.
; TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
; FILE REFERENCE: JHU1630-1
; CURRENT APPLICATION NUMBER: US/10/059,579A
; CURRENT FILING DATE: 2002-01-28
; PRIOR APPLICATION NUMBER: US 09/771,357
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PCR antisense primer
US-10-059-579A-123

Query Match 52.5%; Score 12.6; DB 3; Length 19;
Best Local Similarity 57.9%; Pred. No. 9.1e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 GAGGGCGUGGUUAGGCGU 22
Db 19 GAAGGGGTAGTTAAGGGGT 1

RESULT 11
US-09-166-186-119/c
; Sequence 119, Application US/09166186A
; Patent No. 6080580
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-a EXPRESSION
; FILE REFERENCE: ISPH-0322
; CURRENT APPLICATION NUMBER: US/09/166,186A
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-166-186-119

Query Match 52.5%; Score 12.6; DB 3; Length 20;
Best Local Similarity 63.2%; Pred. No. 9.1e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 GAGGGCGUGGUUAGGCGU 22
Db 20 GGCGGGCGGGTTGAGGGGT 2

RESULT 12
US-09-313-932-119/c
; Sequence 119, Application US/09313932A
; Patent No. 6228642
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-
; FILE REFERENCE: ISPH-0356
; CURRENT APPLICATION NUMBER: US/09/313,932A
; CURRENT FILING DATE: 1999-05-18
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APPLICANT: RODRIGUEZ, IGNACIO R
TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR

Search completed: October 16, 2006, 14:47:12
Job time : 56.5789 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:16:09 ; Search time 337.985 Seconds
(without alignments)
872.534 Million cell updates/sec

Title: US-10-604-726A-6034

Perfect score: 24

Sequence: 1 ugagagggcugguuagggcucc 24

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 23237482

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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Published Applications NA_Main:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
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- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16.6	69.2	25	13	US-11-036-317-713202 Sequence 713202,
C 2	16.2	67.5	25	9	US-10-719-900-888593 Sequence 888593,
C 3	15.8	65.8	24	3	US-09-940-185-365 Sequence 365, App
C 4	15.8	65.8	25	3	US-09-940-185-4341 Sequence 4341, Ap
C 5	15.8	65.8	25	13	US-11-036-317-751276 Sequence 751276,
C 6	15.6	65.0	25	13	US-11-036-317-508584 Sequence 508584,
C 7	15.6	65.0	25	13	US-11-036-317-648052 Sequence 648052,
C 8	15.2	63.3	21	11	US-10-310-914A-310484 Sequence 310484,
C 9	15.2	63.3	21	11	US-10-310-914A-310485 Sequence 310485,
C 10	15.2	63.3	21	11	US-10-310-914A-310486 Sequence 310486,
C 11	15.2	63.3	21	11	US-10-310-914A-310487 Sequence 310487,
C 12	15.2	63.3	21	11	US-10-310-914A-594029 Sequence 594029,
C 13	15.2	63.3	21	11	US-10-310-914A-1286104 Sequence 1286104,
C 14	15.2	63.3	22	11	US-10-310-914A-1056699 Sequence 1056699,
C 15	15.2	63.3	22	11	US-10-310-914A-594065 Sequence 594065,
C 16	15.2	63.3	24	11	US-10-310-914A-1286102 Sequence 1286102,
C 17	15.2	63.3	25	9	US-10-719-900-62329 Sequence 62329, A

18	15.2	63.3	25	15	US-11-121-849-463132 Sequence 463132,
C 19	15	62.5	25	9	US-10-719-900-470368 Sequence 470368,
C 20	15	62.5	25	9	US-10-719-900-473457 Sequence 473457,
C 21	15	62.5	25	13	US-11-036-317-537085 Sequence 537085,
C 22	15	62.5	25	13	US-11-036-317-537085 Sequence 537085,
C 23	15	62.5	25	13	US-11-036-317-537085 Sequence 537085,
C 24	15	62.5	25	13	US-11-036-317-713203 Sequence 713203,
C 25	15	62.5	25	13	US-11-036-317-713203 Sequence 713203,
C 26	15	62.5	25	13	US-11-036-317-713203 Sequence 713203,
C 27	14.8	61.7	21	11	US-10-310-914A-752575 Sequence 752575,
C 28	14.8	61.7	21	11	US-10-310-914A-752575 Sequence 752575,
C 29	14.6	60.8	21	11	US-10-310-914A-371120 Sequence 371120,
C 30	14.6	60.8	21	11	US-10-310-914A-371120 Sequence 371120,
C 31	14.6	60.8	21	11	US-10-310-914A-371120 Sequence 371120,
C 32	14.6	60.8	21	11	US-10-310-914A-371120 Sequence 371120,
C 33	14.6	60.8	21	11	US-10-310-914A-371120 Sequence 371120,
C 34	14.6	60.8	21	11	US-10-310-914A-371120 Sequence 371120,
C 35	14.6	60.8	21	11	US-10-310-914A-371120 Sequence 371120,
C 36	14.6	60.8	21	11	US-10-310-914A-371120 Sequence 371120,
C 37	14.6	60.8	21	11	US-10-310-914A-371120 Sequence 371120,
C 38	14.6	60.8	21	11	US-10-310-914A-371120 Sequence 371120,
C 39	14.6	60.8	21	11	US-10-310-914A-371120 Sequence 371120,
C 40	14.4	60.0	21	12	US-10-504-589A-7 Sequence 7, Appli
C 41	14.4	60.0	21	12	US-10-504-589A-7 Sequence 7, Appli
C 42	14.4	60.0	25	8	US-10-719-956-605791 Sequence 605791,
C 43	14.4	60.0	25	8	US-10-719-956-605792 Sequence 605792,
C 44	14.4	60.0	25	13	US-11-036-317-213436 Sequence 213436,
C 45	14.4	60.0	25	13	US-11-036-317-884459 Sequence 884459,

ALIGNMENTS

RESULT 1

US-11-036-317-713202/c
; Sequence 713202, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 713202
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-713202

Query Match 69.2%; Score 16.6; DB 13; Length 25;
Best Local Similarity 65.2%; Pred. No. 8.8e+02;
Matches 15; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GAGAGGGGUGUUAAGGCGUCC 24

DB 24 GAGAGGGGCGTTCAGGAGTCC 2

RESULT 2

US-10-719-900-888593/c
; Sequence 888593, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Wei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20

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; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 888593
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-888593

Query Match      67.5%; Score 16.2; DB 9; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 GAGGGGCGUGUUAAGGCGUCC 24
Db 23 GAAGGGCTAGTTAAGGCTCC 3

RESULT 3
US-09-940-185-365
; Sequence 365, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 365
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-365

Query Match      65.8%; Score 15.8; DB 3; Length 24;
Best Local Similarity 73.7%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAGGGCGUGUUAAGGC 20
Db 4 GAGAGGCGTTGGTTAAGGC 22

RESULT 4
US-09-940-185-4341
; Sequence 4341, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4341
; LENGTH: 25
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-4341

Query Match      65.8%; Score 15.8; DB 3; Length 25;
Best Local Similarity 73.7%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAGGGCGUGUUAAGGC 20
Db 5 GAGAGGCGTTGGTTAAGGC 23

RESULT 5
US-11-036-317-751276/c
; Sequence 751276, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 751276
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-751276

Query Match      65.8%; Score 15.8; DB 13; Length 25;
Best Local Similarity 68.4%; Pred. No. 2.1e+03;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 UCAGAGGGCGUGUUAAGG 19
Db 25 TCAAAGGGGCGTGGTTAAGG 7

RESULT 6
US-11-036-317-508584/c
; Sequence 508584, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 508584
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-508584

Query Match      65.0%; Score 15.6; DB 13; Length 25;
Best Local Similarity 63.6%; Pred. No. 2.6e+03;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 AGAGGGCGUGUUAAGGCGUCC 24
Db 25 AGAGGCCCTGGTTACGAGGTCC 4
```

```
RESULT 7
US-11-036-317-648052/c
; Sequence 648052, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blums, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 648052
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-648052

Query Match          65.0%; Score 15.6; DB 13; Length 25;
Best Local Similarity 63.8%; Pred. No. 2.6e+03;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY  2  GAGAGGGGCGUGUUAAGGCGUC 23
    |||||  |||  |||  |||  |||  |||
Db  22 GAGAGGCCCTGTTTCAGGATC 1

RESULT 8
US-10-310-914A-310484/c
; Sequence 310484, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 310484
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-310484

Query Match          63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY  1  UGAGAGGGGCGUGUUAAGGC 20
    :|||||  |||  |||  |||  |||
Db  21 TGAGAGGGGAGGCTAAGGC 2

RESULT 9
US-10-310-914A-310485/c
; Sequence 310485, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 310485
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-310485

Query Match          63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY  1  UGAGAGGGGCGUGUUAAGGC 20
    :|||||  |||  |||  |||  |||
Db  21 TGAGAGGGGAGGCTAAGGC 2

RESULT 10
US-10-310-914A-310486/c
; Sequence 310486, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 310486
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-310486

Query Match          63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY  1  UGAGAGGGGCGUGUUAAGGC 20
    :|||||  |||  |||  |||  |||
Db  21 TGAGAGGGGAGGCTAAGGC 2

RESULT 11
US-10-310-914A-310487/c
; Sequence 310487, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 310487
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-310487

Query Match          63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY  1  UGAGAGGGGCGUGUUAAGGC 20
    :|||||  |||  |||  |||  |||
Db  21 TGAGAGGGGAGGCTAAGGC 2
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RESULT 12
US-10-310-914A-594029
; Sequence 594029, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 594029
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-594029

Query Match          63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 85.0%; Pred. No. 4.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GAGAGGGCGUGGUUAGGCG 21
      ||||| ||||| ||||| |||||
DB      2 GAGAGGGCGUGGUUAGGCG 21

RESULT 13
US-10-310-914A-1286104/C
; Sequence 1286104, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1286104
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1286104

Query Match          63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 85.0%; Pred. No. 4.1e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 GAGAGGGCGUGGUUAGGCG 21
      ||||| ||||| ||||| |||||
DB      2 GAGAGGGCGUGGUUAGGCG 21

RESULT 14
US-10-310-914A-1056699/C
; Sequence 1056699, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
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; SEQ ID NO 1056699
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1056699

Query Match          63.3%; Score 15.2; DB 11; Length 22;
Best Local Similarity 80.0%; Pred. No. 4.1e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 GAGAGGGCGUGGUUAGGCG 21
      ||||| ||||| ||||| |||||
DB      21 GAGAGGGCGTGGAGAAGGCG 2

RESULT 15
US-10-310-914A-594065
; Sequence 594065, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 594065
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-594065

Query Match          63.3%; Score 15.2; DB 11; Length 24;
Best Local Similarity 85.0%; Pred. No. 4.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GAGAGGGCGUGGUUAGGCG 21
      ||||| ||||| ||||| |||||
DB      4 GAGAGGGCGUGGUUAGGCG 23

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JOB time : 338.985 secs
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:16:55 ; Search time 53.2331 Seconds
(without alignments)
842.395 Million cell updates/sec

Title: US-10-604-726A-6034

Perfect score: 24
Sequence: 1 uagagggcgguuaagcgucc 24

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 239520 seqs, 934235491 residues

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Maximum DB seq length: 30

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Maximum Match 100%
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Database : Published Applications NA New:
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3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	13.8	57.5	25	8	US-11-217-529-40910 Sequence 40910, A
C 2	13.4	55.8	25	8	US-11-217-529-25472 Sequence 25472, A
C 3	13.4	55.8	25	8	US-11-217-529-101402 Sequence 101402, A
C 4	13.2	55.0	25	8	US-11-217-529-36679 Sequence 36679, A
C 5	13.2	55.0	25	9	US-11-348-413-792144 Sequence 792144, A
C 6	13.2	55.0	25	9	US-11-348-413-877012 Sequence 877012, A
C 7	13	54.2	25	8	US-11-217-529-29983 Sequence 29983, A
C 8	13	54.2	25	8	US-11-217-529-41374 Sequence 41374, A
C 9	13	54.2	25	8	US-11-217-529-88277 Sequence 88277, A
C 10	12.8	53.3	25	8	US-11-217-529-45581 Sequence 45581, A
C 11	12.8	53.3	25	8	US-11-217-529-111977 Sequence 111977, A
C 12	12.8	53.3	25	9	US-11-217-529-177967 Sequence 177967, A
C 13	12.8	53.3	25	9	US-11-348-413-32918 Sequence 32918, A
C 14	12.8	53.3	25	9	US-11-348-413-32919 Sequence 32919, A
C 15	12.8	53.3	25	9	US-11-348-413-32920 Sequence 32920, A
C 16	12.8	53.3	25	9	US-11-348-413-32921 Sequence 32921, A
C 17	12.8	53.3	25	9	US-11-348-413-620816 Sequence 620816, A
C 18	12.8	53.3	25	9	US-11-348-413-620817 Sequence 620817, A
C 19	12.8	53.3	25	9	US-11-348-413-620818 Sequence 620818, A
C 20	12.8	53.3	25	9	US-11-348-413-1233237 Sequence 1233237, A
C 21	12.6	52.5	25	8	US-11-217-529-74782 Sequence 74782, A
C 22	12.6	52.5	25	8	US-11-217-529-113852 Sequence 113852, A
C 23	12.6	52.5	25	9	US-11-348-413-657889 Sequence 657889, A

ALIGNMENTS.

RESULT 1

US-11-217-529-40910/c
; Sequence 40910, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 40910
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-40910

Query Match 57.5%; Score 13.8; DB 8; Length 25;
Best Local Similarity 70.6%; Pred. No. 4.1e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 8 GGCUGGUUAAGCGGUCC 24
|||:|||||
DB 24 GCGTGGTTAAAGCGGCC 8

RESULT 2

US-11-217-529-25472
; Sequence 25472, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

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; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25472
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-25472

Query Match          55.8%; Score 13.4; DB 8; Length 25;
Best Local Similarity 66.7%; Pred. No. 6.3e+03;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 9 GCGUGUUAAGCGCUC 23
   |||::: |||||:|
Db 9 GCTGGTTAGGCGTC 23

RESULT 3
US-11-217-529-101402/c
; Sequence 101402, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 101402
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-101402

Query Match          55.8%; Score 13.4; DB 8; Length 25;
Best Local Similarity 56.5%; Pred. No. 6.3e+03;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 UGAGAGGCGCUGGUUAAGCGCUC 23
   :||| ||| : :||| |
Db 24 TGAGACGGGTAGTTAAGTAGAC 2

RESULT 4
US-11-217-529-36679/c
; Sequence 36679, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
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; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36679
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-36679

Query Match          55.0%; Score 13.2; DB 8; Length 25;
Best Local Similarity 66.7%; Pred. No. 7.8e+03;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGAGGGCGCUGGUUAAGGC 20
   ||||| :|||:|
Db 25 ATAGGGCCTGGTTAAAGC 8

RESULT 5
US-11-348-413-792144
; Sequence 792144, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 792144
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 5316; WAN01UNLH_at; Start 930; Stop 954;
; OTHER INFORMATION: 0000100000000000
US-11-348-413-792144

Query Match          55.0%; Score 13.2; DB 9; Length 25;
Best Local Similarity 66.7%; Pred. No. 7.8e+03;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 AGGGGCGCUGGUUAAGCGU 22
   |||||:|:|
Db 5 AAGGGCTGGTATAGGCGT 22

RESULT 6
US-11-348-413-877012/c
; Sequence 877012, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
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; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 877012
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 7631; WAN01UMIA_at; Start 143; Stop 167;
; OTHER INFORMATION: 00000011100000
US-11-348-413-877012

Query Match      55.0%; Score 13.2; DB 9; Length 25;
Best Local Similarity 72.2%; Pred. No. 7.8e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 AGAGGGCGUGUUAAGGC 20
Db      23 AGATGGCCGATTAAAGC 6

RESULT 7
US-11-217-529-29983/c
; Sequence 29983, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29983
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-29983

Query Match      54.2%; Score 13; DB 8; Length 25;
Best Local Similarity 57.1%; Pred. No. 9.6e+03;
Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      3 AGAGGGCGUGUUAAGGC 23
Db      25 AGAGGGCGTGTTCCTCTTC 5

RESULT 8
US-11-217-529-41374
; Sequence 41374, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
```

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; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 41374
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-41374

Query Match      54.2%; Score 13; DB 8; Length 25;
Best Local Similarity 57.1%; Pred. No. 9.6e+03;
Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      3 AGAGGGCGUGUUAAGGC 23
Db      1 AGTGGCGTGTTCAGGATTC 21

RESULT 9
US-11-217-529-88277
; Sequence 88277, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 88277
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-88277

Query Match      54.2%; Score 13; DB 8; Length 25;
Best Local Similarity 57.1%; Pred. No. 9.6e+03;
Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      3 AGAGGGCGUGUUAAGGC 23
Db      4 AAAGTGGCTGTTCAGGATTC 24

RESULT 10
US-11-217-529-45581
; Sequence 45581, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
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; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45581
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-45581

Query Match      53.3%; Score 12.8; DB 8; Length 25;
Best Local Similarity 75.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGGGCGUGGUUAGG 19
    ||||| :|||: |||
Db 6 GAGGSACTGTCGAAG 21

RESULT 11
US-11-217-529-111977/c
; Sequence 111977, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHITIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIOHKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 111977
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-111977

Query Match      53.3%; Score 12.8; DB 8; Length 25;
Best Local Similarity 54.2%; Pred. No. 1.2e+04;
Matches 13; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 UGAGAGGGCGUGGUUAGGGUCC 24
    :|||: |||: |||: |||
Db 24 TGAGAAACGCTAGTAAACGATCC 1

RESULT 12
US-11-217-529-177967/c
; Sequence 177967, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHITIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIOHKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 177967
; LENGTH: 25
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; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-177967

Query Match      53.3%; Score 12.8; DB 8; Length 25;
Best Local Similarity 62.5%; Pred. No. 1.2e+04;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 8 GCUGGUUAGGGUCC 23
    |||: |||: |||: |||: |
Db 22 GGTGGTTAAGGCATC 7

RESULT 13
US-11-348-413-32918
; Sequence 32918, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 32918
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 423; WAN01UJBU; Start 271; Stop 295;
; OTHER INFORMATION: 111111100000000
US-11-348-413-32918

Query Match      53.3%; Score 12.8; DB 9; Length 25;
Best Local Similarity 62.5%; Pred. No. 1.2e+04;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 UCAGAGGGCGUGGUUA 16
    : |||: |||: |||: |||: |
Db 9 TAAGACGGGCTGGTTA 24

RESULT 14
US-11-348-413-32919
; Sequence 32919, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
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; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 32919
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 423; WAN01UJBU; Start 272; Stop 296;
; OTHER INFORMATION: 11111100000000
US-11-348-413-32919

Query Match 53.3%; Score 12.8; DB 9; Length 25;
Best Local Similarity 62.5%; Pred. No. 1.2e+04;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 UGAGAGGGCGUGGUUA 16
: ||| |||||:|:
Db 8 TAAGACGGGCTGGTTA 23

RESULT 15
US-11-348-413-32920
; Sequence 32920, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 32920
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 423; WAN01UJBU; Start 273; Stop 297;
; OTHER INFORMATION: 11111100000000
US-11-348-413-32920

Query Match 53.3%; Score 12.8; DB 9; Length 25;
Best Local Similarity 62.5%; Pred. No. 1.2e+04;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 UGAGAGGGCGUGGUUA 16
: ||| |||||:|:
Db 7 TAAGACGGGCTGGTTA 22

Search completed: October 16, 2006, 14:22:01
Job time : 53.2331 secs

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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 13:14:58 ; Search time 1370 Seconds
(without alignments)
11762.591 Million cell updates/sec

Title: US-10-604-726A-8797
Perfect score: 252
Sequence: 1 99gtatctgcactgagag.....tctctcttgcacacctcc 252

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 636136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 2862434

Minimum DB seq length: 0
Maximum DB seq length: 120

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

1: gb_env:*
2: gb_pat:*
3: gb_ph:*
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8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	27.8	11.0	98	5	S69137	S69137 Homo sapien
C 2	26.2	10.4	98	5	S69198	S69198 Homo sapien
C 3	25.2	10.0	109	7	AB150733	AB150733 Homo sapi
C 4	24.8	9.8	92	2	BD035734	BD035734 Sequence
C 5	24.8	9.8	92	2	AR735995	AR735995 Sequence
C 6	24.8	9.8	92	2	AX900201	AX900201 Sequence
C 7	24.6	9.8	103	2	CQ471292	CQ471292 Sequence
C 8	24.6	9.8	104	2	CQ480460	CQ480460 Sequence
C 9	24.4	9.7	119	5	AY751306	AY751306 Homo sapi
C 10	24.2	9.6	96	2	AR431314	AR431314 Sequence
C 11	23.8	9.4	78	2	AR477180	AR477180 Sequence
C 12	23.8	9.4	78	2	AR606935	AR606935 Sequence
C 13	23.8	9.4	78	2	AR701924	AR701924 Sequence
C 14	23.6	9.4	72	2	BD034735	BD034735 Sequence
C 15	23.6	9.4	72	2	AR734996	AR734996 Sequence
C 16	23.6	9.4	72	2	AX899202	AX899202 Sequence
C 17	23.6	9.4	97	2	AX184498	AX184498 Sequence
C 18	23.4	9.3	100	2	AX989552	AX989552 Sequence

19	23.4	9.3	100	2	AX996400	AX996400 Sequence
20	23.4	9.3	100	2	CQ874706	CQ874706 Sequence
C 21	23.2	9.2	59	2	E37929	E37929 Remedy for
C 22	23.2	9.2	81	10	AY390010	AY390010 Hepatitis
C 23	23.2	9.2	101	2	CQ149122	CQ149122 Sequence
C 24	23.2	9.2	101	2	CQ232396	CQ232396 Sequence
C 25	23.2	9.2	101	2	CQ307710	CQ307710 Sequence
C 26	23.2	9.2	101	2	CQ344556	CQ344556 Sequence
C 27	23.2	9.2	111	5	HSA012224	HSA012224 Homo sapi
C 28	23	9.1	51	6	AF094482	AF094482 Mus muscu
C 29	23	9.1	54	6	AY177451	AY177451 Mus muscu
C 30	23	9.1	65	2	CQ531157	CQ531157 Sequence
C 31	23	9.1	81	10	AF040860	AF040860 Hepatitis
C 32	23	9.1	120	7	BV012636	BV012636 MS201 Hu
C 33	22.8	9.0	60	2	CQ546820	CQ546820 Sequence
C 34	22.8	9.0	110	5	HSRETINT11	HSRETINT11 Human RET p
C 35	22.6	9.0	66	2	CQ630945	CQ630945 Sequence
C 36	22.6	9.0	66	2	AR472008	AR472008 Sequence
C 37	22.4	8.9	60	6	MUSIGXYZ	MUSIGXYZ Mouse Ig S-
C 38	22.4	8.9	98	6	AF387673	AF387673 Mesocrice
C 39	22.4	8.9	119	2	AX907922	AX907922 Sequence
C 40	22.4	8.9	119	2	BD043455	BD043455 Sequence
C 41	22.4	8.9	119	2	AR743716	AR743716 Sequence
C 42	22.2	8.8	51	2	CQ007958	CQ007958 Sequence
C 43	22.2	8.8	67	2	BD034947	BD034947 Sequence
C 44	22.2	8.8	67	2	AR735208	AR735208 Sequence
C 45	22.2	8.8	67	2	AX899414	AX899414 Sequence

ALIGNMENTS

RESULT 1	S69137/c	S69137	Homo sapiens T-cell receptor alpha-chain (TCR V alpha) mRNA, partial cds.	98 bp	mRNA	linear	PRI 16-MAR-2001
LOCUS	S69137	S69137	Homo sapiens (human)				
DEFINITION	S69137	S69137	Homo sapiens (human)				
ACCESSION	S69137	S69137	Homo sapiens (human)				
VERSION	S69137	S69137	Homo sapiens (human)				
KEYWORDS	S69137	S69137	Homo sapiens (human)				
SOURCE	S69137	S69137	Homo sapiens (human)				
ORGANISM	S69137	S69137	Homo sapiens (human)				
REFERENCE	S69137	S69137	Homo sapiens (human)				
AUTHORS	S69137	S69137	Homo sapiens (human)				
TITLE	S69137	S69137	Homo sapiens (human)				
JOURNAL	S69137	S69137	Homo sapiens (human)				
PUBMED	S69137	S69137	Homo sapiens (human)				
REMARK	S69137	S69137	Homo sapiens (human)				
FEATURES	S69137	S69137	Homo sapiens (human)				
source	S69137	S69137	Homo sapiens (human)				
gene	S69137	S69137	Homo sapiens (human)				
CDS	S69137	S69137	Homo sapiens (human)				
ORIGIN	S69137	S69137	Homo sapiens (human)				

Query Match		11.0%;	Score 27.8;	DB 5;	Length 98;
Best Local Similarity		57.5%;	Pred. No. 1.9e+03;		
Matches 50;		Conservative 0;	Mismatches 37;	Indels 0;	Gaps 0;
QY	65	GTTCCTGAGTGCAGAGTCCTCTGACTCCCTCTGCCACGGGCTGAGTTTCGGCTCCAGG	124		
Db	93	GATATTGGCTTCACAGTGAGCGTAGTCCCAAGGTTGATTGCTGCTGATGGT	34		
QY	125	TTCCGCGTGCCTGAGGTTTGAGGC	151		
Db	33	GGTGCTTGCTGCACAGAAGTAGTGGC	7		
RESULT 2					
S69198/c	S69198	98 bp mRNA linear PRI 06-MAR-2001			
LOCUS	Homo sapiens T-cell receptor alpha-chain (TCR V alpha) mRNA,				
DEFINITION	partial cds.				
ACCESSION	S69198				
VERSION	S69198.1	GI:545963			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
AUTHORS	Hominidae; Homo.				
	1 (bases 1 to 98)				
TITLE	Mohapatra,S.S., Mohapatra,S., Yang,M., Ansari,A.A., Parronchi,P.,				
	Maggi,E. and Romagnani,S.				
JOURNAL	Molecular basis of cross-reactivity among allergen-specific human T				
	cells: T-cell receptor V alpha gene usage and epitope structure				
PUBMED	Immunology 81 (1), 15-20 (1994)				
REMARK	7510663				
FEATURES	GenBank staff at the National Library of Medicine created this				
	entry [NCBI gibbsq 144557] from the original journal article.				
source	Location/Qualifiers				
	1..98				
gene	/organism="Homo sapiens"				
	/mol_type="mRNA"				
CDS	/isolates="grass-sensitive individual VI 17"				
	/db_xref="taxon:9606"				
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Best Local Similarity		56.3%;	Pred. No. 6.2e+03;		
Matches 49;		Conservative 0;	Mismatches 38;	Indels 0;	Gaps 0;
QY	65	GTTCCTGAGTGCAGAGTCCTCTGACTCCCTCTGCCACGGGCTGAGTTTCGGCTCCAGG	124		
Db	93	GATATTGGCTTCACAGTGAGCGTAGTCCCAAGGTTGATTGCTGCTGATGGT	34		
QY	125	TTCCGCGTGCCTGAGGTTTGAGGC	151		
Db	33	GGTGCTTGCTGCACAGAAGTAGTGGC	7		
RESULT 3					
AB150733	AB150733	109 bp DNA linear STS 27-OCT-2005			
LOCUS	Homo sapiens DNA, STS on chromosome 10, D10S08121, sequence tagged				
DEFINITION	site.				
ACCESSION	AB150733				

VERSION	AB150733.1	GI:62171551
KEYWORDS	STS.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Hominidae; Homo.	
REFERENCE	1	
AUTHORS	Tamiya,G., Shinya,M., Imanishi,T., Ikuta,T., Makino,S., Okamoto,K., Furugaki,K., Matsumoto,T., Mano,S., Ando,S., Nozaki,Y., Yukawa,W., Nakashige,R., Yamaguchi,D., Ishibashi,H., Yonekura,M., Nakami,Y., Takayama,S., Endo,T., Saruwatari,T., Yagura,M., Yoshihara,Y., Fujimoto,K., Oka,A., Chiku,S., Linsen,S.E., Giphart,M.J., Kulaki,J.K., Fukazawa,T., Hashimoto,H., Kimura,M., Hoshina,Y., Suzuki,Y., Hotta,T., Mochida,J., Minezaki,T., Komai,K., Shiozawa,S., Taniguchi,A., Yamanaka,H., Kamatani,N., Gojobori,T., Bahram,S. and Inoko,H.	
TITLE	Whole genome association study of rheumatoid arthritis using 27 039 microsatellites	
JOURNAL	Hum. Mol. Genet. 14 (16), 2305-2321 (2005)	
PUBMED	16000323	
REFERENCE	2 (bases 1 to 109)	
AUTHORS	Tamiya,G., Makino,S., Fujimoto,K., Oka,A., Hayashi,H., Denda,A., Linsen,S.E., Ikuta,T., Shinya,M., Endo,T., Tomizawa,M., Tokubo,E., Sato,R., Takaki,A., Nagatsuka,Y., Watanabe,H., Adachi,S., Makino,Y., Nakano,S., Yamamoto,A., Yoshida,K., Okamoto,K., Yamaguchi,D., Ishibashi,H., Yonekura,M., Takayama,S., Nakami,Y., Saruwatari,T., Brand,A., van Hiltten,J.A., van de Watering,L.M., Giphart,M.J., Bahram,S., Kulski,Y.J. and Inoko,H.	
TITLE	Direct Submission	
JOURNAL	Submitted (12-DEC-2003) Hidetoshi Inoko, Tokai University School of Medicine, Department of Genetic Information, Bohseidai, Isehara, Kanagawa, 259-1193, Japan [E-mail:hinoko@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121, Fax:81-463-94-8884]	
COMMENT	Polymorphisms were confirmed by comparing with the pooled DNA typing data of 88 Dutch population or 100 Australian. When there was no significant difference between the Japanese and these Caucasians, individual typing was performed to confirm polymorphisms.	
FEATURES	Location/Qualifiers	
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	1..18	
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repeat_region	51..78	
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	/rpt_type=tandem	
primer_bind	/rpt_unit_seq="cagg"	
	complement(89..109)	
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Qy	138	CTGAGGTTTGAGGCCAGACAGCTCGGCGAGGAGGGCGGGGAGACGAGCGG 197
Db	42	CTGAGTTTTCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAG 101
Qy	198	CT 199
Db	102	CT 103

RESULT 4
BD035734
LOCUS
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD035734
VERSION BD035734.1 GI:22577476
KEYWORDS JP 2001269182-A/11980.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 92)
REFERENCE
AUTHORS Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 11980 02-OCT-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/11980
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EMERIC DUCLAIR,JEAN YVES
PI JORDAN
PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
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CC
FH Key Location/Qualifiers.
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Query Match 9.8%; Score 24.8; DB 2; Length 92;
Best Local Similarity 67.3%; Pred. No. 1.7e+04;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 156 CAGCTCGCAGTCGGCAGGAGCGGGGAGAGACGAGCGGCTCTGGCCCC 207
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Db 13 CAGCTCGAAATCGAGCGGAACAGCGGGCTGGAGCGGGCGGCGGCC 64
RESULT 5
AR735995
LOCUS
DEFINITION Sequence 16064 from patent US 6783961.
ACCESSION AR735995
VERSION AR735995.1 GI:77429735
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 92)
AUTHORS Edwards,J.B.D.M., Duclair,A. and Giordano,J.-Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: US 6783961-A 16064 31-AUG-2004;
GENSET S.A.;
FRX;
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/organism="unknown"
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Best Local Similarity 67.3%; Pred. No. 1.7e+04;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 156 CAGCTCGCAGTCGGCAGGAGCGGGGAGAGACGAGCGGCTCTGGCCCC 207
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RESULT 6
AX900201
LOCUS
DEFINITION Sequence 16064 from Patent EP1033401.
ACCESSION AX900201
VERSION AX900201.1 GI:40055115
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 16064 06-SEP-2000;
GENSET (FR)
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Best Local Similarity 67.3%; Pred. No. 1.7e+04;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
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Db 13 CAGCTCGAAATCGAGCGGAACAGCGGGCTGGAGCGGGCGGCGGCC 64
RESULT 7
CQ471292
LOCUS
DEFINITION Sequence 3158 from Patent WO0160860.
ACCESSION CQ471292
VERSION CQ471292.1 GI:41436911
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Schlegel,R., Endege,W.O. and Monahan,J.E.
TITLE Genes differentially expressed in human prostate cancer and their
JOURNAL use
Patent: WO 0160860-A 3158 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
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ORIGIN
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Best Local Similarity 57.0%; Pred. No. 2e+04;
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QY 234 CTCTCTTTCGCCACTCC 252
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QY 156 CAGCTCGCAGTCGGCAGGAGCGGGGAGAGACGAGCGGCTCTGGCCCC 207
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RESULT 6
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LOCUS
DEFINITION Sequence 16064 from Patent EP1033401.
ACCESSION AX900201
VERSION AX900201.1 GI:40055115
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 16064 06-SEP-2000;
GENSET (FR)
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Query Match 9.8%; Score 24.8; DB 2; Length 92;
Best Local Similarity 67.3%; Pred. No. 1.7e+04;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 156 CAGCTCGCAGTCGGCAGGAGCGGGGAGAGACGAGCGGCTCTGGCCCC 207
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Db 13 CAGCTCGAAATCGAGCGGAACAGCGGGCTGGAGCGGGCGGCGGCC 64
RESULT 7
CQ471292
LOCUS
DEFINITION Sequence 3158 from Patent WO0160860.
ACCESSION CQ471292
VERSION CQ471292.1 GI:41436911
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Schlegel,R., Endege,W.O. and Monahan,J.E.
TITLE Genes differentially expressed in human prostate cancer and their
JOURNAL use
Patent: WO 0160860-A 3158 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
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Best Local Similarity 57.0%; Pred. No. 2e+04;
Matches 45; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 174 GGAGCGCGGGGAGAGACGAGCGGCTCTGGCCCCCTTAATTGACTTCGGGCTGATTGT 233
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Db 2 GGTACGCGGGGAGACGCGCGCGCTCGGAGCTGTAGTGGCTTCGTTGGTTTT 61
QY 234 CTCTCTTTCGCCACTCC 252
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JOURNAL Patent: US 6696256-A 145 24-FEB-2004;
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Qy 169 GGCAGGG 175
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Db 18 GTCAGAG 12

RESULT 12
AR606935/c
LOCUS 78 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 145 from patent US 6821737.
ACCESSION AR606935
VERSION AR606935.1 GI:56659110
KEYWORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 78)
AUTHORS Li, X.
TITLE Method for screening for drug candidates for modulating
transcription factor activity
JOURNAL Patent: US 6821737-A 145 23-NOV-2004;
Panomics, Inc.; Redwood City, CA
FEATURES source
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Qy 169 GGCAGGG 175
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Db 18 GTCAGAG 12

RESULT 13
AR701924/c
LOCUS 78 bp DNA linear PAT 20-SEP-2005
DEFINITION Sequence 145 from patent US 6924113.
ACCESSION AR701924
VERSION AR701924.1 GI:75917786
KEYWORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 78)
AUTHORS Li, X.
TITLE Method and kit for isolating DNA probes that bind to activated
transcription factors
JOURNAL Patent: US 6924113-A 145 02-AUG-2005;
Panomics, Inc.; Redwood City, CA
FEATURES source
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RESULT 14
BD034735/c
LOCUS 72 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD034735
VERSION BD034735.1 GI:22576477
KEYWORDS JP 2001269182-A/10981.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 72)
AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 10981 02-OCT-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/10981
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PJ JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40
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  Best Local Similarity 69.6%; Pred. No. 4e+04;
  Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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RESULT 15
AR734996/c
LOCUS 72 bp DNA linear PAT 11-OCT-2005
DEFINITION Sequence 15065 from patent US 6789961.
ACCESSION AR734996
VERSION AR734996.1 GI:77428736
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
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Unclassified.
REFERENCE 1 (bases 1 to 72)
AUTHORS Edwards J.-B.D.M., Duclert A. and Giordano J.-Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: US 6783961-A 15065 31-AUG-2004;
Genset S.A.;
FRX;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
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Query Match 9.4%; Score 23.6; DB 2; Length 72;
Best Local Similarity 69.6%; Pred. No. 4e+04;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 128 GCCTGTGCGCCCTGAGGTTTGAGGCCACAGACAGCTCGCAGTCGGGCAG 173
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Db 58 GCCTGGGGCCCCGGGGATCGAGGGCATCCAGACACAGAGGGGCCAG 13

Search completed: October 16, 2006, 13:38:02
Job time : 1373 secs

GenCore version 5.1.1.9
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14: Geneseqn2005s.*
15: Geneseqn2006s.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES									
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3	24.6	9.8	103	5	ABV03167	Abv03167	Human pro		
4	24.6	9.8	104	5	ABV12336	Abv12336	Human pro		
5	24.2	9.6	105	4	AAR36160	Aar36160	Human col		
C 6	23.8	9.4	78	8	ABT17318	Abt17318	Transcrip		
C 7	23.6	9.4	72	3	AAC10990	Aac10990	Human sec		
8	23.6	9.4	97	4	AAR68919	Aar68919	Human cer		
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10	23.4	9.3	100	8	ACD76587	Acd76587	E. coli K		
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12	23.4	9.3	100	13	ADR99734	Adr99734	Nucleic a		
C 13	23.2	9.2	59	3	AAR289260	Aar289260	Human emb		
C 14	23.2	9.2	101	4	AAK44587	Aak44587	Human bon		
C 15	23.2	9.2	101	4	AAK18659	Aak18659	Human bra		
C 16	23.2	9.2	101	4	ABS44245	Abs44245	Human liv		
C 17	23.2	9.2	101	6	ABS18824	Abs18824	Human gen		
18	23.2	9.2	118	12	ACH88031	Ach88031	Human gen		

C 19	23	9.1	65	6	ABN28044	Abn28044 Rat splic
C 20	23	9.1	87	6	ABL75509	Ab175509 Corn tase
C 21	22.8	9.0	60	6	ABN43707	Abn43707 Human spl
C 22	22.8	9.0	88	13	ADQ91596	Adq91596 Template
C 23	22.8	9.0	117	9	ADA73750	Ada73750 Carcinoma
C 24	22.6	9.0	66	6	ABN15693	Abn15693 Human gen
C 25	22.6	9.0	66	13	ACN78783	Acn78783 Human GDM
C 26	22.4	8.9	119	3	AAC19710	Aac19710 Human sec
C 27	22.2	8.8	51	4	AAL33390	Aal33390 Human SNP
C 28	22.2	8.8	67	3	AAC11202	Aac11202 Human sec
C 29	22.2	8.8	88	13	ADR50936	Adr50936 Human mus
C 30	22.2	8.8	88	13	ADR50937	Adr50937 Human mus
C 31	22.2	8.8	88	13	ADR50938	Adr50938 Human mus
C 32	22.2	8.8	102	3	AAZ60564	Aaz60564 A neublas
C 33	22.2	8.8	102	6	ABT11892	Abt11892 PCR produ
C 34	22.2	8.8	106	2	AAV46418	Aav46418 Ribosomal
C 35	22.2	8.8	115	3	ACL16203	Acc16203 Human sec
C 36	22.2	8.8	115	9	ACL25369	Acc125369 DNA clone
C 37	22	8.7	68	15	ABE99649	Aee99649 Mouse mir
C 38	22	8.7	89	14	ADX04314	Adx04314 Mouse pri
C 39	22	8.7	93	2	AAQ97727	Aaq97727 Toxoplasm
C 40	22	8.7	102	14	ABE50490	Aeb50490 Human myo
C 41	22	8.7	113	4	ABA36569	Abas36569 Probe #15
C 42	21.8	8.7	61	3	AAZ89261	Aaz89261 Human emb
C 43	21.8	8.7	93	14	ACL68051	Acc168051 M. xanthu
C 44	21.8	8.7	96	6	ABS67407	Abs67407 cDNA enco
C 45	21.8	8.7	96	6	ABS67408	Abs67408 Complemen

ALIGNMENTS

RESULT 1
ABQ76940
ID ABQ76940 standard; DNA; 115 BP.
XX
AC ABQ76940;
XX
DT 27-MAR-2003 (first entry)
DE Polylinker ScaI-Li- (BsgI-ScaI) DNA.
XX
KW Murine; T cell receptor; TCR; hdm2; T cell response; alpha TCR; beta TCR;
KW antigen-recognising sequence; ARS; fusion construct; cytostatic;
KW apoptotic; tumour; leukaemia; immunisation; ds.
OS Synthetic.
XX
PN DE10109854-A1.
XX
PD 12-SEP-2002.
XX
PF 01-MAR-2001; 2001DE-01009854.
XX
PR 01-MAR-2001; 2001DE-01009854.
(STAN/) STANISLAWSKI T.
Theobalt M, Voss H, Stanislawski T;
WPI; 2002-714556/78.
P-PSDB; ABG73655.
New polypeptide of a murine alpha/beta T-cell receptor, useful for
treating tumors and leukemia, induces specific lysis or apoptosis of cells
expressing hdm2 protein.
Example 2; Fig 6; 52pp; German.
This invention describes a novel murine alphabeta T-cell receptor (TCR)
that mediates a hdm2 protein-specific T cell response, a fusion protein
(FP) that includes the TCR and nucleic acid encoding it, alpha or beta-
chains of a TCR that include the antigen-recognizing sequence (ARS) of an

Db 2 GGTACCGGGGAGACCGCGCGCTGCGAGCTGTAGTGGCTTCGCTTCGGTTT 61
QY 234 CTCCTCTTTCGGCACCTCC 252
Db 62 CTCCTCTTCGCTAAGCC 80

RESULT 4
ID ABV12336 standard; cDNA; 104 BP.
AC ABV12336;
XX
XX
DT 13-SEP-2002 (first entry)
XX
XX
DE Human prostate expression marker cDNA 12327.
XX
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200160860-A2.
XX
XX
PD 23-AUG-2001.
XX
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
XX
WPI; 2001-662795/76.
XX

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

Claim 1; Page 2030; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodynamic or pharmacogenomic marker

XX
XX
SQ Sequence 104 BP; 9 A; 39 C; 30 G; 26 T; 0 U; 0 Other;
Query Match 9.8%; Score 24.6; DB 5; Length 104;
Best Local Similarity 57.0%; Pred. No. 2.5e+03;
Matches 45; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 174 GGAGGCGGGGAGACGAGCGGCTCTGGCCCCCTTAATTGTACTTCGGGCTCGTATTCT 233
Db 2 GGTACCGGGGAGACCGCGCGCTGCGAGCTGTAGTGGCTTCGCTTCGGTTT 61
QY 234 CTCCTCTTTCGGCACCTCC 252

Db 62 CTCCTCTTCGCTAAGCC 80

RESULT 5
AAH36160
ID AAH36160 standard; cDNA; 105 BP.
XX
XX
AC AAH36160;
XX
XX
DT 03-SEP-2001 (first entry)
XX
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:3242.
XX
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200122920-A2.
XX
XX
PD 05-APR-2001.
XX
XX
PF 28-SEP-2000; 2000WO-US026524.
XX
XX
PR 29-SEP-1999; 99US-0157137P.
PR 03-NOV-1999; 99US-0163280P.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
XX
WPI; 2001-235357/24.
DR P-PSDB; AAG76755.
XX
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.

Claim 1; Page 5034-5035; 9803pp; English..

XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patient's own production of P. Additionally, N may be used to produce the colon cancer-associated P, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAG77789 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922

XX
XX
SQ Sequence 105 BP; 24 A; 36 C; 32 G; 8 T; 0 U; 5 Other;
Query Match 9.6%; Score 24.2; DB 4; Length 105;
Best Local Similarity 53.7%; Pred. No. 3.2e+03;
Matches 44; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 96 CTGCCACGGCTGAGTTTCCGGCTCCAGGTTCCGCTGCTGAGGTTTCAGGGCAGA 155
Db 24 CCGCNACGCCCCGACGAGNACCGGTCCGGAATCCCGGTGACCCACGCTTTCGCCAA 83
QY 156 CAGCTCGCAGTCGGGACGGAG 177
Db 84 CATGCGGGGACGAGCGGGG 105

RESULT 6
ABT17318/c
ID ABT17318 standard; DNA; 78 BP.
XX AC ABT17318;
XX AC
XX DT 10-APR-2003 (first entry)
XX DE Transcription factor-related array hybridisation probe - SEQ ID NO 145.
XX KW Probe; ss; transcription factor-protein complex; transcription factor;
XX KW drug screening; drug identification; array hybridisation.
XX OS Unidentified.
XX XX
XX PN WO2002101351-A2.
XX PD 19-DEC-2002.
XX PF 30-MAY-2002; 2002WO-US017408.
XX PR 08-JUN-2001; 2001US-00877243.
XX PR 08-JUN-2001; 2001US-00877403.
XX PR 08-JUN-2001; 2001US-00877705.
XX PR 08-JUN-2001; 2001US-00877738.
XX PR 05-SEP-2001; 2001US-00947274.
XX XX
XX PA (PANO-) PANOMICS INC.
XX XX
XX PI Li X;
XX XX
XX DR WPI; 2003-148829/14.
XX XX
XX PT Identifying transcription factor-protein complexes, by isolating
XX PT transcription factor complexes from sample based on a specific type of
XX PT factor, and identifying different proteins present in isolated complexes.
XX PS Disclosure; Fig 6; 167pp; English.
XX XX
XX CC The invention comprises a method for identifying complexes between a
XX CC transcription factor and another protein. The invention also comprises a
XX CC method for isolating DNA probes which bind to activated transcription
XX CC factors. The methods of the invention are useful for identifying
XX CC transcription factor-protein interactions. The methods of the invention
XX CC are also useful for facilitating the screening and identification of new
XX CC drugs, characterising their mechanism of action and screening for adverse
XX CC side effects based on drug's impact expression. The present DNA sequence
XX CC represents a probe used in the method of the invention
XX XX
XX SQ Sequence 78 BP; 15 A; 27 C; 15 G; 21 T; 0 U; 0 Other;
Query Match 9.4%; Score 23.8; DB 8; Length 78;
Best Local Similarity 59.7%; Pred. No. 3.9e+03;
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 109 AGTTTCGGCTCCAGGTTCCGCTGTCGCTGAGGTTTGGCCACACAGCTCGCAGTCG 168
DB 78 AGCTTCAGGTCAGAGGTCAGAGAGTAGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAG 19
QY 169 GGCAGGG 175
DB 18 GTCAGAG 12
RESULT 7
AAC10990/c
ID AAC10990 standard; cdNA; 72 BP.
XX AC AAC10990;
XX DT 06-OCT-2000 (first entry)
XX XX
XX DE Human secreted protein 5' EST, SEQ ID NO: 15065.

XX KW Human; 5' EST; expressed sequence tag; secreted protein; cdNA isolation;
XX KW gene therapy; chromosome mapping; ss.
XX OS Homo sapiens.
XX PN EP1033401-A2.
XX PD 06-SEP-2000.
XX PF 21-FEB-2000; 2000EP-00200610.
XX PR 26-FEB-1999; 99US-0122487P.
XX XX (GEST) GENSET.
XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX DR WPI; 2000-500381/45.
XX XX
XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX PS Claim 1; SEQ ID NO 15065; 71pp + Sequence Listing; English.
XX XX
XX CC The present sequence is one of a large number of 5' ESTs derived from
XX CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
XX CC identified within the present sequence. The 5' ESTs were prepared from
XX CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
XX CC sequences usually correspond mainly to the 3' untranslated region (UTR)
XX CC of the mRNA because they are often obtained from oligo-dT primed cDNA
XX CC libraries. Such ESTs are not well suited for isolating cDNA sequences
XX CC derived from the 5' ends of mRNAs and even in those cases where longer
XX CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
XX CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
XX CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
XX CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX CC They are used to obtain upstream regulatory sequences and to design
XX CC expression and secretion vectors
XX XX
XX SQ Sequence 72 BP; 9 A; 33 C; 20 G; 10 T; 0 U; 0 Other;
Query Match 9.4%; Score 23.6; DB 3; Length 72;
Best Local Similarity 69.6%; Pred. No. 4.4e+03;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 128 GCGTGTCCGCTCGAGGTTTGGCCACACAGCTCGCAGTCGCGGCGAG 173
DB 58 GCGTGGGCGCGGGGATCGAGGGCATCCAGCACAGAGCGCGCCAG 13
RESULT 8
AAH68919
ID AAH68919 standard; cdNA; 97 BP.
XX AC AAH68919;
XX DT 19-SEP-2001 (first entry)
XX XX
XX DE Human cervical cancer marker nucleic acid 193.
XX KW Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX OS Homo sapiens.
XX PN WO200142467-A2.
XX PD 14-JUN-2001.
XX PF 08-DEC-2000; 2000WO-US033312.
XX PR 08-DEC-1999; 99US-0169681P.

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PR 21-DEC-1999; 99US-0171350P.
PR 14-MAR-2000; 2000US-0189315P.
PR 12-MAY-2000; 2000US-0203791P.
PR 09-JUN-2000; 2000US-0210600P.
PR 21-JUL-2000; 2000US-0220114P.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Deeds J, Berger A, Zhao X;
XX WPI; 2001-375006/39.
XX New isolated nucleic acid for diagnosing and treating cervical cancer and
PT for assessing and detecting compounds for treating the cancer.
XX Claim 1; Page 137; 1051pp; English.
XX The invention relates to novel genes (AAH68727-AAH73383) associated with
CC cervical cancer with cytostatic activity. The nucleic acids and encoded
CC polypeptides are useful: to assess if a patient is afflicted with
CC cervical cancer or has a pre-malignant condition; to monitor the
CC progression of cervical cancer or a premalignant condition in a patient;
CC and to select and/or assess the efficacy of a compound or therapy for
CC inhibiting cervical cancer in a patient. The nucleic acids may also be
CC useful for gene therapy
XX
XX Sequence 97 BP; 7 A; 34 C; 30 G; 23 T; 0 U; 3 Other;
SQ
Query Match 9.4%; Score 23.6; DB 4; Length 97;
Best Local Similarity 59.4%; Pred. No. 4.8e+03;
Matches 38; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 189 GACGAGCGGCTCTGGCCCTTAATTGTACTTCGGGCTCGPATGTCTCTCTCTTCGCCAC 248
DB 6 GCCGAGGTACCGCGGGGCTGNAGTAGGCTTCGTCCTCGGNTTCTCTCTCTCTCGCTAA 65
QY 249 CTCC 252
DB 66 CGCC 69
RESULT 9
ACD69745/C
ID ACD69745 standard; DNA; 100 BP.
XX
AC ACD69745;
XX
DT 18-SEP-2003 (first entry)
XX
XX E. coli K12 MG1655 biochip probe SEQ ID 1015.
XX Biochip; gene expression; gut; diagnostic; detection; probe; ss.
XX Escherichia coli.
XX
XX EP1260592-A1.
XX
XX 27-NOV-2002.
XX
XX 17-MAY-2001; 2001EP-00112179.
XX
XX 17-MAY-2001; 2001EP-00112179.
XX (MWGB-) MWG-BIOTECH AG.
XX
XX Donner H, Drescher B, Huber A, Weber J;
XX WPI; 2003-241155/24.
XX
XX Biochip containing probes complementary with open reading frames in
PT Escherichia coli K12, useful for detecting gene expression and expression
XX patterns.
XX
PR 21-DEC-1999; 99US-0171350P.
PR 14-MAR-2000; 2000US-0189315P.
PR 12-MAY-2000; 2000US-0203791P.
PR 09-JUN-2000; 2000US-0210600P.
PR 21-JUL-2000; 2000US-0220114P.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Deeds J, Berger A, Zhao X;
XX WPI; 2001-375006/39.
XX New isolated nucleic acid for diagnosing and treating cervical cancer and
PT for assessing and detecting compounds for treating the cancer.
XX Claim 1; Page 137; 1051pp; English.
XX The invention relates to novel genes (AAH68727-AAH73383) associated with
CC cervical cancer with cytostatic activity. The nucleic acids and encoded
CC polypeptides are useful: to assess if a patient is afflicted with
CC cervical cancer or has a pre-malignant condition; to monitor the
CC progression of cervical cancer or a premalignant condition in a patient;
CC and to select and/or assess the efficacy of a compound or therapy for
CC inhibiting cervical cancer in a patient. The nucleic acids may also be
CC useful for gene therapy
XX
XX Sequence 97 BP; 7 A; 34 C; 30 G; 23 T; 0 U; 3 Other;
SQ
Query Match 9.4%; Score 23.6; DB 4; Length 97;
Best Local Similarity 59.4%; Pred. No. 4.8e+03;
Matches 38; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 189 GACGAGCGGCTCTGGCCCTTAATTGTACTTCGGGCTCGPATGTCTCTCTCTTCGCCAC 248
DB 6 GCCGAGGTACCGCGGGGCTGNAGTAGGCTTCGTCCTCGGNTTCTCTCTCTCTCGCTAA 65
QY 249 CTCC 252
DB 66 CGCC 69
RESULT 9
ACD69745/C
ID ACD69745 standard; DNA; 100 BP.
XX
AC ACD69745;
XX
DT 18-SEP-2003 (first entry)
XX
XX E. coli K12 MG1655 biochip probe SEQ ID 1015.
XX Biochip; gene expression; gut; diagnostic; detection; probe; ss.
XX Escherichia coli.
XX
XX EP1260592-A1.
XX
XX 27-NOV-2002.
XX
XX 17-MAY-2001; 2001EP-00112179.
XX
XX 17-MAY-2001; 2001EP-00112179.
XX (MWGB-) MWG-BIOTECH AG.
XX
XX Donner H, Drescher B, Huber A, Weber J;
XX WPI; 2003-241155/24.
XX
XX Biochip containing probes complementary with open reading frames in
PT Escherichia coli K12, useful for detecting gene expression and expression
XX patterns.
XX
PS Claim 3; Page 168; 2004pp; German.
XX This invention describes a novel biochip comprising probe spots, each
CC containing many identical probes. The probes are nucleotide sequences of
CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
CC least one includes a segment of at least 20 bases identical with, or
CC complementary to, a segment of an open reading frame (orf) of Escherichia
CC coli K12. The biochip is used for specific detection of gene expression
CC in K12 and for determining the gene expression pattern, e.g. for
CC diagnostic determination of which E. coli strains are present in the gut,
CC and to determine the effects of e.g. growth media on gene expression. The
CC biochip provides as comprehensive as possible detection of the K12
CC genome, with simultaneous analysis of many different genes with a single
CC device, and comparison of gene expression between K12 and its mutants or
CC other E. coli strains in a single experiment. Apart from qualitative and
CC quantitative information about gene expression, it also allows
CC measurements of population densities for the various strains. The use of
CC synthetic oligonucleotides for preparation of probes allows free
CC variation in probe length and ensures high purity (and thus selectivity,
CC reactivity and reproducibility); also synthetic probes are generally
CC shorter than probes prepared by polymerase chain reaction. ACD68731 to
CC ACD81540 represent oligonucleotide probes used with the biochip described
CC in the invention
XX
XX Sequence 100 BP; 21 A; 29 C; 38 G; 12 T; 0 U; 0 Other;
SQ
Query Match 9.3%; Score 23.4; DB 8; Length 100;
Best Local Similarity 63.2%; Pred. No. 5.5e+03;
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 100 CACGGCTGAGTTTCGGCTCCAGGTTCCGGTTCGGTTCGCCCTTGAGTTTGAGCCAGAC 156
DB 88 CAAGTTCTGCGCGCTGCACCATGTTCCAGTGCCTGCGCGGGTTTCTGCGCAGCC 32
RESULT 10
ACD76587
ID ACD76587 standard; DNA; 100 BP.
XX
AC ACD76587;
XX
DT 18-SEP-2003 (first entry)
XX
XX E. coli K12 MG1655 biochip probe SEQ ID 7863.
XX
XX Biochip; gene expression; gut; diagnostic; detection; probe; ss.
XX Escherichia coli.
XX
XX EP1260592-A1.
XX
XX 27-NOV-2002.
XX
XX 17-MAY-2001; 2001EP-00112179.
XX
XX 17-MAY-2001; 2001EP-00112179.
XX (MWGB-) MWG-BIOTECH AG.
XX
XX Donner H, Drescher B, Huber A, Weber J;
XX WPI; 2003-241155/24.
XX
XX Biochip containing probes complementary with open reading frames in
PT Escherichia coli K12, useful for detecting gene expression and expression
XX patterns.
XX
PS Claim 3; Page 1228; 2004pp; German.
XX This invention describes a novel biochip comprising probe spots, each
CC containing many identical probes. The probes are nucleotide sequences of
CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
CC least one includes a segment of at least 20 bases identical with, or

```



```
SQ Sequence 100 BP; 15 A; 36 C; 25 G; 24 T; 0 U; 0 Other;
Query Match          9.3%; Score 23.4; DB 13; Length 100;
Best Local Similarity 63.2%; Pred. No. 5.5e+03;
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 100 CACGGCTGAGTTCCGGCTCCAGGTTCCGCTGCGCCCTGAGGTTGAGGCCAGAC 156
DB 12 CAAGTTCTGCGCGCTGCACCATGTTGCGCAGTGCAGCGCGGTTTCTGGCCAGCC 68

RESULT 13
AAZ89260/C
ID AAZ89260 standard; DNA; 59 BP.
XX
AC AAZ89260;
XX
DT 09-JUN-2000 (first entry)
XX
DE Human embryonic brain protein PCR primer #5.
XX
KW Human; brain; nerve degeneration; nootropic; neuroprotective;
KW anticonvulsant; antiparkinsonian; antidiabetic; treatment; infarction;
KW Parkinson's disease; Alzheimer's disease; Huntington's disease;
KW muscular hypoplastic lateral sclerosis; diabetic neuropathy; PCR primer;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200007614-A1.
XX
PD 17-FEB-2000.
XX
PF 02-AUG-1999; 99WO-JP004171.
XX
PR 05-AUG-1998; 98JP-00221886.
PR 05-FEB-1999; 99JP-00029164.
XX
PA (SAKA) OTSUKA PHARM CO LTD.
XX
PI Horie M, Hirano H, Kyushiki H, Mitsumoto Y, Mori A, Watanabe A;
XX
WPI; 2000-205568/18.
XX
New protein isolated from human embryonic brain useful for treating nerve
degeneration diseases e.g. Parkinson's diseases and Alzheimer's disease.
XX
Example 2; Page 62; 69pp; Japanese.
XX
This invention describes a novel human embryonic brain derived protein
(I) which has nootropic, neuroprotective, anticonvulsant,
antiparkinsonian and antidiabetic activity. (I) is useful for treating
nerve degeneration diseases e.g. Parkinson's disease, Alzheimer's
disease, muscular hypoplastic lateral sclerosis, Huntington's disease,
brain infarction, diabetic neuropathy and traumatic nerve degeneration.
CC AAZ89256-289234 represent PCR primers used in the isolation and
CC amplification of the human brain protein described in the method of the
CC invention
XX
SQ Sequence 59 BP; 9 A; 23 C; 14 G; 13 T; 0 U; 0 Other;
Query Match          9.2%; Score 23.2; DB 3; Length 59;
Best Local Similarity 65.4%; Pred. No. 5.5e+03;
Matches 34; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 159 CTCGAGTCTGGCAGGAGGGGGGAGAGAGCAGCGGCTCTGGCCCTTA 210
DB 52 CTGGCAGTCTGCTCAGGAGGTCGGGAAAGCAGCCAGCTTTAAGCGGCGCATA 1

RESULT 14
AAK44587/c
ID AAK44587 standard; DNA; 101 BP.
```

```
XX
AC AAK44587;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 19144.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000668.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
(MOLE-) MOLECULAR DYNAMICS INC.
XX
Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-489900/53.
XX
Human genome-derived single exon nucleic acid probes useful for analyzing
gene expression in human bone marrow.
XX
Example 4; SEQ ID NO 19144; 658pp + Sequence Listing; English.
XX
The present invention provides a number of single exon nucleic acid
probes which are derived from genomic sequences expressed in the human
bone marrow. They can be used to measure gene expression in bone marrow
samples, which may enable the improved diagnosis and treatment of cancers
such as lymphoma, leukaemia and myeloma. The present sequence is one of
the probes of the invention
XX
SQ Sequence 101 BP; 36 A; 22 C; 23 G; 20 T; 0 U; 0 Other;
Query Match          9.2%; Score 23.2; DB 4; Length 101;
Best Local Similarity 61.7%; Pred. No. 6.3e+03;
Matches 37; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 27 GTTAAGGGCTCCCAAGTTGGAAGGGCGCTTGTCTTCTGATGCGAGAGTCTC 86
DB 64 GCTGAGTCATAACCTGCTTCAAGCAGACTGGGTTTCTGATTCTGATGCGCAGAGTCTC 5

RESULT 15
AAK18659/c
ID AAK18659 standard; DNA; 101 BP.
XX
AC AAK18659;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 18650.
XX
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
```

PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234887P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX
PS Example 4; SEQ ID NO 18650; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system,
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
SQ Sequence 101 BP; 36 A; 22 C; 23 G; 20 T; 0 U; 0 Other;

Query Match 9.2%; Score 23.2; DB 4; Length 101;
Best Local Similarity 61.7%; Pred. No. 6.3e+03;
Matches 37; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 27 GTTAAGCGTCCCAAGTTGGAGGGCGTTTCTTCTGTTCTGATGCAGATCCTC 86
Db 64 GCTGATCATACCTGCTTCAAGACAGACTGGGTTTCTGATTTCTGATGCAGATCCTC 5

Search completed: October 16, 2006, 13:14:41
Job time : 257 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 13:38:19 ; Search time 2284 Seconds
(without alignments)
6169.734 Million cell updates/sec

Title: US-10-604-726A-8797

Perfect score: 252

Sequence: 1 ggggtatctgcaactgagag.....tctctcttccacacctcc 252

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 1484138

Minimum DB seq length: 0

Maximum DB seq length: 120

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1:	gb_est1:*
2:	gb_est3:*
3:	gb_est4:*
4:	gb_est5:*
5:	gb_est6:*
6:	gb_hic:*
7:	gb_est3:*
8:	gb_est7:*
9:	gb_est8:*
10:	gb_est9:*
11:	gb_ges1:*
12:	gb_ges2:*
13:	gb_ges3:*
14:	gb_ges4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	11.5	100	11	AZ769498
2	27.6	11.0	103	12	CG574657
3	26.2	10.4	82	12	CG535738
C 4	25.8	10.2	110	5	CK014560
C 5	25.8	10.2	110	13	CL952591
6	25.6	10.2	99	7	AV841732
7	25.6	10.2	103	13	DU408432
C 8	25.6	10.2	117	12	CG255380
C 9	25.2	10.0	103	7	AW800261
C 10	25	9.9	100	10	DV900899
C 11	25	9.9	108	11	AZ697609
C 12	24.8	9.8	89	2	BG718505
13	24.8	9.8	116	12	BZ836170
14	24.8	9.8	120	14	CNS02660
15	24.6	9.8	107	4	CB219192
16	24.6	9.8	119	12	BZ987003
C 17	24.4	9.7	95	2	BF724320
C 18	24.4	9.7	109	10	DV552589
19	24.4	9.7	119	9	DN773586

C	20	24.2	9.6	104	8	CN071764
	21	24.2	9.6	115	13	CW117487
	22	24.2	9.6	117	13	DU188381
	23	24	9.5	92	12	BZ585533
	24	24	9.5	100	5	CK005996
C	25	24	9.5	100	13	CL952595
	26	24	9.5	101	4	CD029354
	27	24	9.5	102	12	CC376448
	28	24	9.5	105	5	CK451897
	29	24	9.5	116	5	CF741809
C	30	23.8	9.4	93	5	CK100624
	31	23.8	9.4	101	2	BJ965328
	32	23.8	9.4	102	2	BJ965717
	33	23.8	9.4	102	2	BJ970068
	34	23.8	9.4	103	2	BJ967675
C	35	23.8	9.4	109	2	BJ967592
	36	23.8	9.4	109	2	BJ968752
	37	23.8	9.4	116	7	AW619414
	38	23.8	9.4	117	2	BJ554385
	39	23.8	9.4	120	1	AJ924324
C	40	23.6	9.4	108	4	CB221358
	41	23.6	9.4	109	7	AW493199
	42	23.6	9.4	113	11	AZ922634
	43	23.4	9.3	79	8	CN868873
	44	23.4	9.3	104	8	CO018108
45	23.4	9.3	106	2	BG994249	

ALIGNMENTS

RESULT 1
AZ769498
LOCUS
DEFINITION
1M0570K16F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0570K16 F, genomic survey sequence.
ACCESSION
AZ769498
VERSION
AZ769498.1
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

GI:12889695

100 bp DNA linear GSS 16-FEB-2001

1 (bases 1 to 100)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhauser, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dduan@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0570 row: K column: 16

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 100.

Location/Qualifiers

1..100

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="CS7BL/6J"

/db_xref="taxon:10090"

/clone="UUGCIM0570K16"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: pMD22nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD22 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 11.5%; Score 29; DB 11; Length 100;
 Best Local Similarity 71.7%; Pred. No. 3.3e+03;
 Matches 38; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 147 GAGCGACAGACGCTCGAGTCGGGAGGAGGGCGGGGAGACAGCGGCT 199

Db 23 GCGCGAGGTGAGCGCTCCGCCCGGGGAGAGCGGGGAGCGGCGGCT 75

RESULT 2

CG574657 103 bp mRNA linear GSS 02-OCT-2003
 LOCUS OST207730 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST207730,
 DEFINITION mRNA sequence.

ACCESSION CG574657.1 GI:37364994

VERSION GSS.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 103)

Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
 Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
 Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
 Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
 Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
 Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
 Zhu,Q., Person,C. and Sands,A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

14610273

Contact: Zambrowicz BP

OmniBank

Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap.

FEATURES

source

1. .103
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST207730"
 /cell_type="embryonic stem cell"

ORIGIN

Query Match 11.0%; Score 27.6; DB 12; Length 103;
 Best Local Similarity 67.2%; Pred. No. 8e+03;
 Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 39 CCAAGTTGGAAGGGCGCTTGTCTCTGTTTCTGGATGCAGAGTCTCTGACTCCCTC 96

Db 42 CCACTTGATAGACACTCTGAGGTTCTTTTGGATCAAGCGTCTTACTGCTTC 99

RESULT 3

CG535738 82 bp mRNA linear GSS 01-OCT-2003
 LOCUS OST122945 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST122945,
 DEFINITION mRNA sequence.

ACCESSION CG535738

VERSION CG535738.1 GI:37322310

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 82)

AUTHORS

Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
 Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
 Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
 Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
 Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
 Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
 Zhu,Q., Person,C. and Sands,A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

14610273

Contact: Zambrowicz BP

OmniBank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap.

FEATURES

source

1. .82
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST122945"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 10.4%; Score 26.2; DB 12; Length 82;
 Best Local Similarity 56.6%; Pred. No. 1.9e+04;
 Matches 43; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 64 TGTCTTCTGGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGCTGAGTTCCGGCTCCAG 123

Db 6 TGTCTTCTTGTCCAAAGATCTCTCANACACTTAGCCACCAACTAGGCANCTACNCCAG 65

QY 124 GTTCGGTGTGCGCCCT 139

Db 66 CTTGATATGAGGCCCT 81

RESULT 4

CK014560/c 110 bp mRNA linear EST 04-FEB-2005
 LOCUS 33148rsicaf_6492.y1 Oryza sativa cv. PA64s panicle sterile cDNA
 DEFINITION

library Oryza sativa (indica cultivar-group) cDNA 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CK014560
CK014560.1 GI:58604032
EST.

Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS

Yu, J., Wang, J., Lin, W., Li, S., Li, H., Zhou, J., Ni, P., Dong, W., Hu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X., Zheng, H., Cong, L., Lin, L., Yin, J., Geng, J., Li, G., Shi, J., Liu, J., Lv, H., Li, J., Wang, J., Deng, Y., Ran, L., Shi, X., Wang, X., Wu, Q., Li, C., Ren, X., Wang, J., Wang, X., Li, D., Liu, D., Zhang, X., Ji, Z., Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, J., Chen, P., Wu, S., and Liu, J.

The Genomes of Oryza sativa: A History of Duplications
PLOS Biol. 3 (2), e38 (2005)

TITLE
JOURNAL
PubMed

15685292
Contact: Yan Zhou
Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China

Tel: 86-571-56805886

Fax: 86-571-56805884

Email: zhouyan@genomics.org.cn

Seq primer: M13 Forward

High quality sequence stop: 110

POLYA=No.

FEATURES
source

1..110

/organism="Oryza sativa (indica cultivar-group)"

/mol_type="mRNA"

/cultivar="PA64s"

/db_xref="taxon:39946"

/tissue_type="panicle"

/cell_type="sterile"

/dev_stage="heading/flowering"

/clone_lib="Oryza sativa cv. PA64s panicle sterile cDNA library"

ORIGIN

Query Match

Best Local Similarity 10.2%; Score 25.8; DB 5; Length 110;

Mismatches 0; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 127

CGCGTGTCCCTGAGGTTTGAGCCGAGACAGCTCCAGTCGGCGAGGCGGGGGA 186

Db 77

CGCCAGCCGCTTACGTTGAGGCGCCACATGGCGCGGAGATGGGGAGGA 18

QY 187

GAGACGAGC 195

Db 17

GAGAGAAGC 9

RESULT 5

LOCUS

OSIRUA001748 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.

ACCESSION

CL952591

CL952591.1 GI:52364600

KEYWORDS

GSS

SOURCE

Oryza sativa (indica cultivar-group)

Oryza sativa (indica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 110)

Ma, L., Wang, J., Chen, C., Liu, X., Sun, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,

TITLE

JOURNAL

COMMENT

Unpublished (2004)

Contact: Chen Chen

Department of Bioinformatic

Beijing Institute of Genomics

Chinese Academy of Sciences, Beijing 101300, China

Tel: 86-10-80481559

Fax: 86-10-80488676

Email: chenchen@genomics.org.cn

Rice genomic sequence.

Class: exon-trapped.

FEATURES

source

1..110

/organism="Oryza sativa (indica cultivar-group)"

/mol_type="genomic DNA"

/db_xref="taxon:39946"

/clone_lib="Oryza sativa Express Library"

/note="Oryza sativa exon trapped genomic sequences"

ORIGIN

Query Match

Best Local Similarity 10.2%; Score 25.8; DB 13; Length 110;

Mismatches 42; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 127

CGCGTGTCCCTGAGGTTTGAGCCGAGACAGCTCCAGTCGGCGAGGCGGGGGA 186

Db 77

CGCCAGCCGCTTACGTTGAGGCGCCACATGGCGCGGAGATGGGGAGGA 18

QY 187

GAGACGAGC 195

Db 17

GAGAGAAGC 9

RESULT 6

LOCUS

AV841732 Nori Satoh unpublished cDNA library, egg ciona intestinalis cDNA clone rcieg05m22, mRNA sequence.

ACCESSION

AV841732

AV841732.1 GI:16785883

KEYWORDS

EST.

SOURCE

Ciona intestinalis

Ciona intestinalis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Cionidae; Ciona.

REFERENCE

AUTHORS

Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.

Expressed genes in Ciona intestinalis

Unpublished (2000)

JOURNAL

COMMENT

Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES

source

1..99

/organism="Ciona intestinalis"

/mol_type="mRNA"

/db_xref="taxon:7719"

/clone="rcieg05m22"

/tissue_type="whole animal"

/dev_stage="egg"

/clone_lib="Nori Satoh unpublished cDNA library, egg"

ORIGIN

Query Match

Best Local Similarity 10.2%; Score 25.6; DB 7; Length 99;

Mismatches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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QY      8  CTCGAACGTAGAGGGCTGTTAAGCGCTCCCAAGTTCGAAGGGCGCTTTTGCTTC 63
Db      16  CTTGCTGTAAGTGGGTTGAATGGGTTTCCCAACATTTGAGGTCACTTTGCTTC 71

RESULT 7
DU0408432
LOCUS   103 bp      DNA      linear      GSS 05-OCT-2005
DEFINITION 1098474026684 CHORI-243 Ovis aries genomic clone CH243-202P18,
genomic survey sequence.
ACCESSION DU0408432
VERSION   DU0408432.1 GI:77138562
KEYWORDS GSS.
SOURCE   Ovis aries (sheep)
ORGANISM Ovis aries
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
          Pecora; Bovidae; Caprinae; Ovis.
REFERENCE 1 (bases 1 to 103)
AUTHORS   Kirkness, E., Shetty, J., de Jong, P., McEwan, J. C., Oddy, H. and
          Cockett, N.
TITLE     Ovine BAC End Sequences from Library CHORI-243
JOURNAL   Unpublished (2004)
COMMENT   Other GSSs: 1098474028028
          Contact: Ewen Kirkness
          The Institute for Genomic Research (TIGR: www.tigr.org)
          9712 Medical Center Drive, Rockville, MD 20850, USA
          Tel: 301-795-7536
          Email: ekirknes@tigr.org
          Sequences generated at the J. Craig Venter Institute Joint
          Technology Center (JCVI/JTC: http://www.venterlinstitute.org/).
          Original Trace: 1098474026684 Trace TI: gnl[ti]918952333
          Insert Length: 184000 Std Error: 0.00 row: P column: 18
          Seq primer: SP6
          Clas: BAC ends.
          Location/Qualifiers
            1..103
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              /mol_type="genomic DNA"
              /strain="Texel breed"
              /db_xref="taxon:9940"
              /clone="CH243-202P18"
              /sex="Male"
              /cell_type="Blood"
              /clone_lib="CHORI-243"
              /notes="vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
              The CHORI-243 sheep (M) (Ovis aries) BAC library produced
              by Pieter de Jong's lab at CHORI
              http://bacpac.chori.org/library.php?id=162"

ORIGIN
Query Match 10.2%; Score 25.6; DB 13; Length 103;
Best Local Similarity 55.7%; Pred. No. 2.9e+04;
Matches 49; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY      64  TGTGTTTCGGATGCAGAGTCCTCTGACTCCCTCGACGCGGCTGAGTTCCGGCTCCAG 123
Db      4   TGTGTTCAAATGCAGAAATCAGAAATGTACATTTCCCATTTCCGAGCTCGGGTACGCGGCCGG 63

QY      124 GTTCGGCGTGTGCGCCCTCGAGGTTTGAGGC 151
Db      64  GGTGGGGGGGAGGCTGGGGTGGAGGC 91

RESULT 8
CG255380/c
LOCUS   117 bp      DNA      linear      GSS 25-AUG-2003
DEFINITION OGVCPE92TH ZM 0.7.1.5 KB Zea mays genomic clone ZMMBMA0505P16,
genomic survey sequence.
ACCESSION CG255380
VERSION   CG255380.1 GI:34159750
KEYWORDS GSS.
SOURCE   Zea mays
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Zea.
          1 (bases 1 to 117)
          Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
          Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
          Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
          Consortium for Maize Genomics
          Unpublished (2002)
          Contact: Cathy Whitelaw
          TIGR
          9712 Medical Center Drive, Rockville, MD 20850, USA
          Tel: 301-838-5843
          Fax: 301-838-0208
          Email: whitelaw@tigr.org
          Seq primer: TR
          Class: methylation filtered.
          Location/Qualifiers
            1..117
              /organism="Zea mays"
              /mol_type="genomic DNA"
              /strain="B73"
              /db_xref="taxon:4577"
              /clone="ZMMBMA0505P16"
              /clone_lib="ZM 0.7.1.5 KB"
              /note="Vector: pBOSK; Site 1: HincII; 0.7-1.5 kb
              methylation filtered genomic DNA library"

ORIGIN
Query Match 10.2%; Score 25.6; DB 12; Length 117;
Best Local Similarity 57.5%; Pred. No. 2.9e+04;
Matches 46; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY      128 GCGTGTCCGCTGAGGTTTGAGGCCGACAGCTCCAGTCGCGGAGGAGCGGGGGAG 187
Db      104 GCGGTCCGGCCAGCGATGTGAAGCACGCGCGGACATCTCGGTCTCGGGGGCCGCCCAG 45

QY      188 AGACGAGCGGCTCTGCGCCCC 207
Db      44 CGATGTGAAGCTCCGGCCTC 25

RESULT 9
AW800261/c
LOCUS   103 bp      mRNA      linear      EST 16-MAY-2000
DEFINITION MR2-UM0060-170400-203-e06 UM0060 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW800261
VERSION   AW800261.1 GI:7852131
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homiidae; Homo.
          1 (bases 1 to 103)
          Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
          Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P.,
          Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bais, G.S., Simpson, D.H.,
          Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
          O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
          Simpson, A.J.
          Shotgun sequencing of the human transcriptome with ORF expressed
          sequence tags
          Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
          10737800
          Contact: Simpson A.J.G.
          Laboratory of Cancer Genetics
          Ludwig Institute for Cancer Research
          Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
          Brazil
          Tel: +55-11-2704922
          Fax: +55-11-2707001

```

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=et2=MR2-UM0060-170
400-203-e06&t3=2000-04-17&t4=1)

Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 80.

FEATURES

source
1. .103
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="UM0060"

/note="Organ: uterus; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 10.0%; Score 25.2; DB 7; Length 103;
Best Local Similarity 55.8%; Pred. No. 3.7e+04;
Matches 48; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 149 GGCCACAGCTCGCAGTCGGGAGGAGGCGGGGAGAGAGCGGCTCTGGCCCT 208
|||||
Db 90 GGCCACAACTCCGACTGGGTGGAGTCGAGGTGGAGGAGTGCCAGACATC 31
|||||

QY 209 TAATTGCTACTCGGCTCGTATTGTC 234
|||||

Db 30 CTTCATAGCCAGGTAACGTTTGTG 5
|||||

RESULT 10

DV900899/c
LOCUS
DEFINITION DV900899 100 bp mRNA linear EST 01-DEC-2005
POS0605016 F07R porcine skeletal muscle cDNA library (POSM) Sus
scrofa cDNA 3', mRNA sequence.

ACCESSION DV900899
VERSION DV900899.1 GI:82926410
KEYWORDS EST.
SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE 1 (bases 1 to 100)
Ernst,C.W., Saama,P.M., Raney,N.E., Lin,S. and Roe,B.A.

Sequencing of ESTs from a normalized porcine skeletal muscle cDNA library

Unpublished (2005)

Contact: Ernst CW
Animal Science Molecular Genetics Lab

Michigan State University
B220 Anthony Hall, East Lansing, MI 48824, USA

Tel: 517 432 1941

Fax: 517 353 1699

Email: ernstc@msu.edu

mRNA sequence

Insert Length: 100 Std Error: 0.00.

Location/Qualifiers

1. .100

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/sex="male and female"

/tissue_type="skeletal muscles"

/dev_stage="45 d and 90 d of gestation, birth, 7 wk and 1 yr of age"

FEATURES

source

ORIGIN

Query Match 9.9%; Score 25; DB 10; Length 100;
Best Local Similarity 56.8%; Pred. No. 4.2e+04;
Matches 46; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 128 GCGTCGCGCCCTGAGGTTTGAGGCCACAGACAGCTCGCAGTCGGGACGAGGCGGGGAG 187
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Db 90 GCTTATCTTTTATTGTTTCTGTCCAGAGCCCTCGCAGTGGGGAGGCGGAGTCGCGGG 31
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QY 188 AGACGAGCGGCTCTGGCCCT 208
|||||

Db 30 AGGTGCGCACCTGCGCACCT 10
|||||

RESULT 11

AZ697609/c

LOCUS

DEFINITION

RPCI-23-240H23-TV RPCI-23 Mus musculus genomic clone

AZ697609

VERSION AZ697609.1 GI:12413877

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 108)

AUTHORS

Zhao,S., Nierman,W., Feidblyum,T., Malek,J., Shatsman,S.,
Akinret,B., Levine,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de
Jong,P. and Fraser,C.M.

Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999)

Other GSSs: RPCI-23-240H23.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong

(pdejong@mail.cho.org). Clones may be purchased from BACPAC

Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end

page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 240 row: H column: 23

Seq primer: T7

Class: BAC ends.

FEATURES

source

1. .108

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-23-240H23"

/sex="Female"

/lab_host="DH10B"

/clone_lib="RPCI-23"

/note="Organ: Kidney/Brain; Vector: pBACE3.6; Site 1:
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACE3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN

```

Query Match      9.9%; Score:25; DB 11; Length 108;
Best Local Similarity 69.4%; Pred.No. 4.2e+04;
Matches 34; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 59 GCTTCTGTTTCTGATGACAGTCTCTGACTCTCCTCTGCCACGGGCT 107
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 90 GCTTCTTCTTACTCTGCGCAGAGGCTCAGGCTCTCTCTCACGCGGCT 42

RESULT 12
BG718505/c
LOCUS      BG718505      89 bp      mRNA      linear      EST 08-MAY-2001
DEFINITION 602696562F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4828574 5',
            mRNA sequence.
ACCESSION  BG718505
VERSION     BG718505
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1 (bases 1 to 89)
AUTHORS    NIH-MGC http://mgi.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strauberg, Ph.D.
            Email: cgabs-k@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10746 row: 1 column: 15
            High quality sequence stop: 19.

FEATURES             Location/Qualifiers
     source           1..89
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4828574"
                     /lab_host="DH108"
                     /clone_lib="NIH_MGC_97"
                     /notes="Organ: testis; Vector: pBluescriptR (modified
                     pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTVN-3', size-selected for average
                     insert size 2.2 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation). Library constructed by M. Brownstein
                     (NIH/NHGRI, National Institutes of Health). Note: this is
                     a NIH_MGC Library."

ORIGIN
Query Match      9.8%; Score 24.8; DB 2; Length 89;
Best Local Similarity 57.9%; Pred.No. 4.7e+04;
Matches 44; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 124 GTTCGGGTGTCGCCCTTGTGAGCCAGACAGCTCGCAGTCGGGCGAGGCGCGG 183
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 76 GTGAGTGGGGTGTCTGTGGGTGGGGCGGCTGTGCTCCCTGGGCGCGGAGCGCGG 17

QY 184 GGAGAGCAGACGGCT 199
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 16 GCGAGGGTAGCCGCT 1

RESULT 13
BZ836170
LOCUS      BZ836170      116 bp      DNA      linear      GSS 18-MAR-2003
DEFINITION CH240_225C14.TJ CHORI-240 Bos taurus genomic clone CH240_225C14,
            genomic survey sequence.
ACCESSION  BZ836170
VERSION     BZ836170.1 GI:29063528
KEYWORDS    GSS.
SOURCE      Bos taurus (cattle)
ORGANISM    Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1 (bases 1 to 116)
AUTHORS    Zhao,S., Shetty,J., Shateman,S., Tsegaye,G., Geer,K.,
            Shvartsbeyn,A., Gebregeorgis,E., Chen,D., Riggs,F., de Jong,P.,
            Crawford,A.M. and McEwan,J.C. Library CHORI-240
            Bovine BAC End Sequences from
            Unpublished (2003)
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the bovine BAC library CHORI-240
            (http://www.chori.org/bacpac/bovine240.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/ordering_information.htm). This work
            was undertaken as part of the International Bovine BAC Mapping
            Consortium (IBBMC) by AgResearch Ltd., New Zealand and The
            Institute of Genomic Research (TIGR), USA.
            Plate: 225 row: C column: 14
            Seq primer: SP6
            Class: BAC ends.

FEATURES             Location/Qualifiers
     source           1..116
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /strain="breed: Hereford"
                     /db_xref="taxon:9913"
                     /clone="CH240_225C14"
                     /sex="Male"
                     /cell_type="Blood"
                     /clone_lib="CHORI-240"
                     /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
                     Hereford bull 11 Domino 99375; CHORI-240 Bovine BAC
                     library (Male) produced by Pieter de Jong"

ORIGIN
Query Match      9.8%; Score 24.8; DB 12; Length 116;
Best Local Similarity 63.3%; Pred.No. 4.9e+04;
Matches 38; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 140 GAGGTTTTCAGGCGCAGACAGCTCGCAGTCGGGCGAGCGGCGGAGAGACGAGCGGCT 199
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 36 GAGATATGAGACCAAGTACCCGGGAGGGGAGGGGCTGCGAGAGGAGGAT 95

RESULT 14
CNS02660
LOCUS      CNS02660      120 bp      DNA      linear      GSS 01-SEP-2000
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            240C22 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION  AL182961
VERSION     AL182961.1 GI:7821065
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
            Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;


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Result No.	Score	Query			DB	ID	Description
		Match	Length	%			
1	24.8	9.8	92	3	US-09-513-999C-16064	Sequence 16064, A	
2	24.2	9.6	96	3	US-09-210-305C-1	Sequence 1, Appli	
C 3	23.8	9.4	78	3	US-09-877-243A-145	Sequence 145, App	
C 4	23.8	9.4	78	3	US-09-877-705A-145	Sequence 145, App	
C 5	23.8	9.4	78	3	US-09-877-738C-145	Sequence 145, App	
C 6	23.6	9.4	72	3	US-09-513-999C-15065	Sequence 15065, A	
C 7	22.6	9.0	66	3	US-09-866-108A-15685	Sequence 15685, A	
8	22.4	8.9	119	3	US-09-513-999C-23785	Sequence 23785, A	
9	22.2	8.8	67	3	US-09-513-999C-15277	Sequence 15277, A	
C 10	22.2	8.8	102	3	US-09-347-611C-13	Sequence 13, Appl	
C 11	22.2	8.8	102	3	US-09-662-183A-13	Sequence 13, Appl	
C 12	22.2	8.8	113	3	US-09-367-927A-1	Sequence 1, Appli	
C 13	22.2	8.8	115	3	US-09-513-999C-20278	Sequence 20278, A	
C 14	21.8	8.7	86	2	US-07-964-624D-57	Sequence 57, Appl	
C 15	21.8	8.7	86	2	US-08-442-062-57	Sequence 57, Appl	
C 16	21.8	8.7	86	2	US-08-748-697A-57	Sequence 57, Appl	
C 17	21.8	8.7	86	3	US-09-165-616-57	Sequence 57, Appl	
C 18	21.8	8.7	86	3	US-10-040-497-57	Sequence 57, Appl	
C 19	21.8	8.7	93	3	US-09-902-540-4514	Sequence 4514, Ap	
C 20	21.8	8.7	104	3	US-09-513-999C-29691	Sequence 29691, A	
C 21	21.8	8.7	107	3	US-09-621-976-9492	Sequence 9492, A	
C 22	21.6	8.6	151	3	US-09-513-999C-14603	Sequence 14603, A	
C 23	21.6	8.6	116	2	US-08-458-423A-34	Sequence 34, Appl	

```
; COUNTRY: U.S.A.
; ZIP: 06510-2802
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM
; OPERATING SYSTEM: WINDOWS 95/98
; SOFTWARE: MS WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,305C
; FILING DATE: 11-Dec-1998
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-210-305C-1

Query Match          9.6%; Score 24.2; DB 3; Length 96;
Best Local Similarity 43.5%; Pred. No. 5.6e+02;
Matches 30; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

QY 32 GCGTCCCAAGTTGGAAGGCGCTTGTCTGTTTCTGATGCAGAGTCTCTGACT 91
DB 10 GCGCGCUGCAAGUGAAUUGCGCUGUCUGUCGACGCGCCUGGCGUGGACUGCCU 69

QY 92 CCCTCTGCC 100
DB 70 GCUGCUGCC 78

RESULT 3
US-09-877-243A-145/c
; Sequence 145, Application US/09877243A
; Patent No. 6696256
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
; FILE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: 26757-702
; CURRENT APPLICATION NUMBER: US/09/877,243A
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
; LENGTH: 78
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP74
US-09-877-243A-145

Query Match          9.4%; Score 23.8; DB 3; Length 78;
Best Local Similarity 59.7%; Pred. No. 7e+02;
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 109 AGTTTCCGGCTCCAGGTTCCGCTGTCGCCCTCAGGTTTGAGGCCAGACAGCTCGCAGTCG 168
DB 78 AGCTTCAGGTCAGAGGTCAGAGGCTAGCTTCAGGTCAGAGGTCAGAGGCTAGCTTCAG 19

QY 169 GGCAGGG 175
DB 18 GTCAGAG 12

RESULT 4
US-09-877-705A-145/c
; Sequence 145, Application US/09877705A
; Patent No. 6821737
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
```

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; TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPT1
; TITLE OF INVENTION: FACTOR ACTIVITY
; FILE REFERENCE: 26757-704
; CURRENT APPLICATION NUMBER: US/09/877,705A
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
; LENGTH: 78
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP74
US-09-877-705A-145

Query Match          9.4%; Score 23.8; DB 3; Length 78;
Best Local Similarity 59.7%; Pred. No. 7e+02;
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 109 AGTTTCCGGCTCCAGGTTCCGCTGTCGCCCTCAGGTTTGAGGCCAGACAGCTCGCAGTCG 168
DB 78 AGCTTCAGGTCAGAGGTCAGAGGCTAGCTTCAGGTCAGAGGTCAGAGGCTAGCTTCAG 19

QY 169 GGCAGGG 175
DB 18 GTCAGAG 12

RESULT 5
US-09-877-738C-145/c
; Sequence 145, Application US/09877738C
; Patent No. 6924113
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
; FILE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: 26757-701
; CURRENT APPLICATION NUMBER: US/09/877,738C
; CURRENT FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
; LENGTH: 78
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP74
US-09-877-738C-145

Query Match          9.4%; Score 23.8; DB 3; Length 78;
Best Local Similarity 59.7%; Pred. No. 7e+02;
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 109 AGTTTCCGGCTCCAGGTTCCGCTGTCGCCCTCAGGTTTGAGGCCAGACAGCTCGCAGTCG 168
DB 78 AGCTTCAGGTCAGAGGTCAGAGGCTAGCTTCAGGTCAGAGGTCAGAGGCTAGCTTCAG 19

QY 169 GGCAGGG 175
DB 18 GTCAGAG 12

RESULT 6
US-09-513-999C-15065/c
; Sequence 15065, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
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Qy 86 CTGACTCCCTCTGCCACGGGTGAGTTTCCGGTCCAGGTTCCGGTGTGCCCC 138

RESULT 10
US-09-347-613C-13/c

```
; Sequence 13, Application US/09347613C
; Patent No. 6593133
; GENERAL INFORMATION:
; APPLICANT: Johansen, Teit E.
; APPLICANT: Blom, Nikolaj
; APPLICANT: Hansen, Claus
; TITLE OF INVENTION: No. 6593133el Neurotrophic Factors
; FILE REFERENCE: NeuroSearch 19313-001
; CURRENT APPLICATION NUMBER: US/09/347,613C
; CURRENT FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: DANISH 1998 00904
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: USSN 60/092,229
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: DANISH 1998 01048
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: USSN 60/097,774
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: DANISH 1998 01260
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: USSN 60/103,908
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: DANISH 1998 01265
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-347-613C-13

Query Match      8.8%; Score 22.2; DB 3; Length 102;
Best Local Similarity 61.0%; Pred. No. 2.4e+03;
Matches 36; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 149 GGCACAGAGCTCGCAGTCGGGCGAGGAGGGGGGAGAGAGAGCGGCTCTGGGCCC 207
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 74 GGCACAGGGCTGGCTGACGGGCGGAGGCCGGGGGGCGGTCCGACGGGCCCCGGGCCC 16

RESULT 11
US-09-662-183A-13/c
; Sequence 13, Application US/09662183A
; Patent No. 6734284
; GENERAL INFORMATION:
; APPLICANT: Johansen, Teit E.
; APPLICANT: Blom, Nikolaj
; APPLICANT: Hansen, Claus
; TITLE OF INVENTION: No. 6734284el Neurotrophic Factors
; FILE REFERENCE: 19313-001 DIV
; CURRENT APPLICATION NUMBER: US/09/662,183A
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: DANISH 1998 00904
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: USSN 60/092,229
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: DANISH 1998 01048
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: USSN 60/097,774
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: DANISH 1998 01260
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: USSN 60/103,908
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: DANISH 1998 01265
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 09/347,613
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-347-613C-13

Query Match      8.8%; Score 22.2; DB 3; Length 102;
Best Local Similarity 61.0%; Pred. No. 2.4e+03;
Matches 36; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 149 GGCACAGAGCTCGCAGTCGGGCGAGGAGGGGGGAGAGAGAGCGGCTCTGGGCCC 207
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 74 GGCACAGGGCTGGCTGACGGGCGGAGGCCGGGGGGCGGTCCGACGGGCCCCGGGCCC 16

RESULT 12
US-09-367-927A-1/c
; Sequence 1, Application US/09367927A
; Patent No. 6300126
; GENERAL INFORMATION:
; APPLICANT: GRUMMT, INGRID
; APPLICANT: RAINWEG, MITTLERER
; APPLICANT: GRUMMT, FRIEDERICK
; APPLICANT: VAN DER VOGELWEIDE STRASSE, WALTHER
; TITLE OF INVENTION: EXPRESSION VECTOR FOR THE PERMANENT
; TITLE OF INVENTION: EXPRESSION OF FOREIGN DNA
; FILE REFERENCE: 35280043US00
; CURRENT APPLICATION NUMBER: US/09/367,927A
; CURRENT FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 113
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-367-927A-1

Query Match      8.8%; Score 22.2; DB 3; Length 113;
Best Local Similarity 64.7%; Pred. No. 2.4e+03;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 147 GAGGCCACAGCTCGCAGTCGGGCGAGGAGGGGGGAGAGAGAGCGG 197
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 66 GTGGCCCCCGCTCCGCGCGGGGGGGGGGGGGGGGAGACACTTTCG 16

RESULT 13
US-09-513-999C-20278/c
; Sequence 20278, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 20278
; LENGTH: 115
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-20278

Query Match      8.8%; Score 22.2; DB 3; Length 115;
Best Local Similarity 61.0%; Pred. No. 2.4e+03;
Matches 36; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 169 GGCAGGAGGGGGGAGAGAGCGGCTCTGGCCCTTAATTGTTACTTTCGGGCTCG 227
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Db 63 GGGTGGGGCCCGGAGAGACAGCACCTCGAGCCAGAAATTGTTTCGCTTCG 5

RESULT 14

US-07-964-624D-57/c
; Sequence 57, Application US/07964624D
; Patent No. 5496938
; GENERAL INFORMATION:
; APPLICANT: GOLD, LARRY M.
; APPLICANT: TURK, CRAIG
; TITLE OF INVENTION: METHOD OF SELECTING NUCLEIC
; TITLE OF INVENTION: ACIDS ON THE BASIS OF
; TITLE OF INVENTION: STRUCTURE
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/5 inch, 1.44 MB
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/964,624D
; FILING DATE: 21-OCTOBER-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX05
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3333
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-964-624D-57

Query Match 8.7%; Score 21.8; DB 2; Length 86;
Best Local Similarity 56.2%; Pred. No. 3e+03;
Matches 41; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 84 CTCTGACTCCCTCGCCAGGGCTGAGTTTCGGGCTCCAGGTTCCGGGTGTCGCCCTTGAGG 143
Db 86 CCGGATCCTCTTTACCTCTGTGAGCTCCAGAGTCCACTATCGTGTTCGATGGAG 27
QY 144 TTTGAGGCCAGAC 156
Db 26 TTGTCGGAAGGC 14

RESULT 15

US-08-442-062-57/c
; Sequence 57, Application US/08442062
; Patent No. 5595877
; GENERAL INFORMATION:
; APPLICANT: GOLD, LARRY M.
; APPLICANT: TURK, CRAIG
; TITLE OF INVENTION: METHOD OF SELECTING NUCLEIC
; TITLE OF INVENTION: ACIDS ON THE BASIS OF

; TITLE OF INVENTION: STRUCTURE
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/5 inch, 1.44 MB
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,062
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX05/D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-442-062-57

Query Match 8.7%; Score 21.8; DB 2; Length 86;
Best Local Similarity 56.2%; Pred. No. 3e+03;
Matches 41; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 84 CTCTGACTCCCTCGCCAGGGCTGAGTTTCGGGCTCCAGGTTCCGGGTGTCGCCCTTGAGG 143
Db 86 CCGGATCCTCTTTACCTCTGTGAGCTCCAGAGTCCACTATCGTGTTCGATGGAG 27
QY 144 TTTGAGGCCAGAC 156
Db 26 TTGTCGGAAGGC 14

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Job time : 125 secs

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OM nucleic - nucleic search, using sw model

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Perfect score: 252
Sequence: 1 99gtatctgcactgagag.....tctctcttcgccacctcc 252

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14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
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16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	27	10.7	67	11 US-10-310-914A-16611	Sequence 16611, A
C 2	25.2	10.0	96	16 US-11-173-902-22	Sequence 22, Appl
C 3	25.2	10.0	109	9 US-10-674-124A-16551	Sequence 16551, A
C 4	24.6	9.8	103	9 US-10-357-930-3158	Sequence 3158, A
C 5	24.6	9.8	104	9 US-10-357-930-12327	Sequence 12327, A
C 6	24.2	9.6	105	6 US-10-106-698-3252	Sequence 3252, A
C 7	24	9.5	93	11 US-10-310-914A-17067	Sequence 17067, A
C 8	23.8	9.4	78	3 US-09-877-705A-145	Sequence 145, App
C 9	23.8	9.4	78	3 US-09-877-274-145	Sequence 145, App
C 10	23.8	9.4	78	3 US-09-877-738A-145	Sequence 145, App
C 11	23.8	9.4	78	4 US-09-877-403A-145	Sequence 145, App
C 12	23.8	9.4	78	4 US-10-779-595-145	Sequence 145, App
C 13	23.4	9.3	100	10 US-10-781-499-1	Sequence 1, Appl
C 14	23.4	9.3	120	3 US-09-796-692-6323	Sequence 6323, Ap
C 15	23.4	9.3	120	6 US-10-040-862-6323	Sequence 6323, Ap
C 16	23.4	9.3	120	7 US-10-057-475B-6323	Sequence 6323, Ap
C 17	23.4	9.3	120	7 US-10-154-884B-6323	Sequence 6323, Ap

18	23.4	9.3	120	9 US-10-764-324-6323	Sequence 6323, Ap
C 19	23.2	9.2	101	3 US-09-864-761-27544	Sequence 27544, A
C 20	23.2	9.2	118	7 US-10-029-386-21226	Sequence 21226, A
C 21	23	9.1	65	3 US-09-908-975-792	Sequence 792, App
C 22	23	9.1	87	3 US-09-294-093B-4883	Sequence 4883, Ap
C 23	22.8	9.0	60	3 US-09-908-975-16455	Sequence 16455, A
C 24	22.6	9.0	66	3 US-09-866-108-15685	Sequence 15685, A
C 25	22.6	9.0	66	8 US-10-723-361-15685	Sequence 15685, A
C 26	22.2	8.9	116	9 US-10-425-115-142012	Sequence 142012, A
C 27	22.2	8.8	102	3 US-09-804-615-13	Sequence 13, Appl
C 28	22.2	8.8	102	8 US-10-661-984A-13	Sequence 13, Appl
C 29	22.2	8.8	102	9 US-10-806-793-13	Sequence 13, Appl
C 30	22	8.7	68	10 US-10-490-955-387	Sequence 387, App
C 31	22	8.7	68	11 US-10-310-914A-2865	Sequence 2865, Ap
C 32	22	8.7	68	11 US-10-310-914A-3692	Sequence 3692, Ap
C 33	22	8.7	89	10 US-10-909-125-1425	Sequence 1425, Ap
C 34	22	8.7	99	11 US-10-310-914A-817	Sequence 817, App
C 35	22	8.7	104	8 US-10-242-535A-9222	Sequence 9222, Ap
C 36	22	8.7	104	8 US-10-085-783A-9222	Sequence 9222, Ap
C 37	22	8.7	113	3 US-09-864-761-21889	Sequence 21889, A
C 38	22	8.7	116	11 US-10-310-914A-12025	Sequence 12025, A
C 39	21.8	8.7	63	11 US-10-310-914A-20336	Sequence 20336, A
C 40	21.8	8.7	86	6 US-10-040-497-57	Sequence 57, Appl
C 41	21.8	8.7	86	9 US-10-818-954-57	Sequence 57, Appl
C 42	21.8	8.7	96	3 US-09-918-063-32	Sequence 32, Appl
C 43	21.8	8.7	96	3 US-09-918-063-34	Sequence 34, Appl
C 44	21.8	8.7	111	3 US-09-864-761-23937	Sequence 23937, A
C 45	21.8	8.7	113	3 US-09-933-797-725	Sequence 725, App

ALIGNMENTS

RESULT 1

US-10-310-914A-16611/c
; Sequence 16611, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuvzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16611
; LENGTH: 67
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-16611

Query Match 10.7%; Score 27; DB 11; Length 67;
Best Local Similarity 85.7%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 30; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 174 GGAGGCGGGGAGAGACGAGCGGCTCTGCCCCCT 208

DB 67 GGAGGCGTGGGAGAGAGAGACCCCTGCCCCCT 33

RESULT 2

US-11-173-902-22/c
; Sequence 22, Application US/11173902
; Publication No. US20060057611A1
; GENERAL INFORMATION:
; APPLICANT: KAO, H. PIN
; APPLICANT: JONES, ROBERT
; TITLE OF INVENTION: LOG-LINEAR AMPLIFICATION
; FILE REFERENCE: 375461-021US
; CURRENT APPLICATION NUMBER: US/11/173,902

PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12327
LENGTH: 104
TYPE: DNA
ORGANISM: Homo sapiens
US-10-357-930-12327

Query Match 9.8%; Score 24.6; DB 9; Length 104;
Best Local Similarity 57.0%; Pred. No. 1.2e+03;
Matches 45; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 174 GGAGGGGGGGGAGACGCGCTCTGCCCCCTTAATTGTACTTCGGGCTCGTATTGT 233
DB 2 GGTACGGGGGAGACGCGCGCGCTGCGACGCTGTAGTGGCTTCGTCCTCGGTTTTT 61

QY 234 CTCCTCTTTCGCCACCTCC 252
DB 62 CTCCTCTTCGCTAACGCC 80

RESULT 6
US-10-106-698-3252
Sequence 3252, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 3252
LENGTH: 105
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (28)..(28)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (40)..(40)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (53)..(53)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (72)..(72)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (77)..(77)
OTHER INFORMATION: n equals a.t.g, or c
US-10-106-698-3252

Query Match 9.6%; Score 24.2; DB 6; Length 105;
Best Local Similarity 53.7%; Pred. No. 1.6e+03;
Matches 44; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 96 CTGCCACGGGCTGAGTTTCGGCTCCAGGTTCCGCTGTCGCTGAGGTTTGAGGCGCAGA 155
DB 24 CCGCNACGCCCGCAGGNACCGGTCCGGAANTCCGGGTGACCCACGCTTCNGCCAAA 83

QY 156 CAGCTCGCAGTCGGCGACGGAG 177
DB 84 CATGGCGGGCAGGACGGGGG 105

RESULT 7
US-10-310-914A-17067
Sequence 17067, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiller, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 17067
LENGTH: 93
TYPE: RNA
ORGANISM: Human
US-10-310-914A-17067

Query Match 9.5%; Score 24; DB 11; Length 93;
Best Local Similarity 51.8%; Pred. No. 1.9e+03;
Matches 29; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY 126 TCGGTGTGCGCTGAGTTTGAGGCGACAGTCGTCAGTCGGCAGGAGGGCG 181
DB 38 UCGGUUUCACCCGUGUUUUGCGGAGAGGCGUGUCCCGUGCGGGGGCG 93

RESULT 8
US-09-877-705A-145/c
Sequence 145, Application US/09877705A
Publication No. US20030008283A1
GENERAL INFORMATION:
APPLICANT: Li, Jason
TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPT
TITLE OF INVENTION: FACTOR ACTIVITY
FILE REFERENCE: 26757-704
CURRENT APPLICATION NUMBER: US/09/877,705A
CURRENT FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PatentIn version 3.1
SEQ ID NO 145
LENGTH: 78
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Hybridization probe MP74
US-09-877-705A-145

Query Match 9.4%; Score 23.8; DB 3; Length 78;
Best Local Similarity 59.7%; Pred. No. 2.1e+03;
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 109 AGTTTCGGCTCCAGTTCGCTGTCGCTGAGGTTTGAGGCGCAGCAGCTCGAGTCG 168
DB 78 AGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAGGTCAGAGGTCAGAGGCTAGCTTCAG 19
QY 169 GGCAGGG 175

Db 18 GTCAGAG 12

RESULT 9

US-09-947-274-145/c
; Sequence 145, Application US/09947274
; Publication No. US20030017499A1
; GENERAL INFORMATION:

; APPLICANT: Li, Xianqiang
; TITLE OF INVENTION: METHOD FOR DETECTING TRANSCRIPTION FACTOR-PROTEIN INTERACTIONS

; FILE REFERENCE: 26757-705
; CURRENT APPLICATION NUMBER: US/09/947,274

; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 09/877,738

; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,243

; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,403

; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,705

; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 162

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145

; LENGTH: 78
; TYPE: DNA

; ORGANISM: Artificial sequence
; FEATURE:

; OTHER INFORMATION: Hybridization probe MP74
US-09-947-274-145

Query Match 9.4%; Score 23.8; DB 3; Length 78;
Best Local Similarity 59.7%; Pred. No. 2.1e+03;

Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 109 AGTTTCGGGCTCCAGGTTCCGCGTGTCCGCTTGGAGGTTTGAGGCCAGACAGCTCGCAGTCG 168

Db 78 AGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTTCAGGTCAGAGGTCAGAGGCTAGCTTTCAG 19

QY 169 GGCAGGG 175

Db 18 GTCAGAG 12

RESULT 10

US-09-877-738A-145/c
; Sequence 145, Application US/0987738A
; Publication No. US20030022173A1
; GENERAL INFORMATION:

; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED

; FILE REFERENCE: 26757-701
; CURRENT APPLICATION NUMBER: US/09/877,738A

; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 162

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145

; LENGTH: 78
; TYPE: DNA

; ORGANISM: Artificial sequence
; FEATURE:

; OTHER INFORMATION: Hybridization probe MP74
US-09-877-738A-145

Query Match 9.4%; Score 23.8; DB 3; Length 78;
Best Local Similarity 59.7%; Pred. No. 2.1e+03;

Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 109 AGTTTCGGGCTCCAGGTTCCGCGTGTCCGCTTGGAGGTTTGAGGCCAGACAGCTCGCAGTCG 168

Db 78 AGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTTCAGGTCAGAGGTCAGAGGCTAGCTTTCAG 19

QY 169 GGCAGGG 175

Db 18 GTCAGAG 12

RESULT 11

US-09-877-403A-145/c
; Sequence 145, Application US/09877403A
; Publication No. US20040214166A1
; GENERAL INFORMATION:

; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD FOR IDENTIFYING A DISEASE STATE BASED ON A DETECTED MIXTURE

; FILE REFERENCE: 26757-703
; CURRENT APPLICATION NUMBER: US/09/877,403A

; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 162

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145

; LENGTH: 78
; TYPE: DNA

; ORGANISM: Artificial sequence
; FEATURE:

; OTHER INFORMATION: Hybridization probe MP74
US-09-877-403A-145

Query Match 9.4%; Score 23.8; DB 4; Length 78;
Best Local Similarity 59.7%; Pred. No. 2.1e+03;

Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 109 AGTTTCGGGCTCCAGGTTCCGCGTGTCCGCTTGGAGGCCAGACAGCTCGCAGTCG 168

Db 78 AGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTTCAGGTCAGAGGTCAGAGGCTAGCTTTCAG 19

QY 169 GGCAGGG 175

Db 18 GTCAGAG 12

RESULT 12

US-10-779-595-145/c
; Sequence 145, Application US/10779595
; Publication No. US20040132090A1
; GENERAL INFORMATION:

; APPLICANT: Li, Xianqiang
; TITLE OF INVENTION: METHOD, ARRAY AND KIT FOR DETECTING ACTIVATED TRANSCRIPTION FACTOR

; FILE REFERENCE: 26757-702.301
; CURRENT APPLICATION NUMBER: US/10/779,595

; CURRENT FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 09/877,243

; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 162

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145

; LENGTH: 78
; TYPE: DNA

; ORGANISM: Artificial sequence
; FEATURE:

; OTHER INFORMATION: Hybridization probe MP74
US-10-779-595-145

Query Match 9.4%; Score 23.8; DB 8; Length 78;
Best Local Similarity 59.7%; Pred. No. 2.1e+03;

Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 109 AGTTTCGGGCTCCAGGTTCCGCGTGTCCGCTTGGAGGCCAGACAGCTCGCAGTCG 168

Db 78 AGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTTCAGGTCAGAGGTCAGAGGCTAGCTTTCAG 19

QY 169 GGCAGGG 175

Db 18 GTCAGAG 12

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RESULT 13
US-10-781-499-1
; Sequence 1, Application US/10781499
; Publication No. US20050054060A1
; GENERAL INFORMATION:
; APPLICANT: Metabolic Explorer
; TITLE OF INVENTION: Method for the preparation of an evolved microorganism for the ch
; TITLE OF INVENTION: or modification of metabolic pathways
; FILE REFERENCE: D20701/ 345774
; CURRENT APPLICATION NUMBER: US/10/781,499
; CURRENT FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: FR 0301924
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: FR 0305768
; PRIOR FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: FR 0305769
; PRIOR FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: FR 0313054
; PRIOR FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Dmeter
US-10-781-499-1

Query Match          9.3%; Score 23.4; DB 10; Length 100;
Best Local Similarity 63.2%; Pred. No. 3e+03;
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 100 CAGCGCTGATTCGGCTCCAGTTCGGTCCGCTCGCTCGCCCTGAGGTTTGAGGCCAGAC 156
DB 12 CAAGTTCTGCGCCCTGCACCATGTTCCGCCAGTGGCGCGGGTTTCTGCGCCAGCC 68

RESULT 14
US-09-796-692-6323
; Sequence 6323, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
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; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6323
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-6323

Query Match          9.3%; Score 23.4; DB 3; Length 120;
Best Local Similarity 60.0%; Pred. No. 3e+03;
Matches 39; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 141 AGGTTTGAGGCCAGACAGCTCGAGTCGCGGCGAGGAGCGCGGGGAGAGACGACGCGGCTC 200
DB 53 AGGTTTGATGCAAGATGCTCTGGGAAGTGCCACGACATATGGGGGAGAAAAGCTGCTC 112

QY 201 TGGCC 205
DB 113 AGACC 117

RESULT 15
US-10-040-862-6323
; Sequence 6323, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6323
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-6323
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Query Match 9.3%; Score 23.4; DB 6; Length 120;
Best Local Similarity 60.0%; Pred. No. 3e+03;
Matches 39; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
Qy 141 AGGTTTGAGGCCAGACAGCTCGCAGTCGGGCGAGGGCGGGGAGAGACGAGCGGCTC 200
Db 53 AGGTTTGATGCAAGATGCTCTGGGAAGTGCACGACAGATATGGGGGAGAGAAAGCTGCTC 112
Qy 201 TGGCC 205
Db 113 AGACC 117

Search completed: October 16, 2006, 13:57:18
Job time : 815 secs

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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 13:43:59 ; Search time 1855 Seconds
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2395520 seqs, 934235491 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22	8.7	102	7	US-11-043-824-258
C 2	21.2	8.4	98	9	US-11-365-556-82
C 3	21	8.3	47	7	US-11-370-584-3264
C 4	21	8.3	103	8	US-11-266-748A-424752
C 5	20.8	8.3	106	8	US-11-266-748A-307408
C 6	20.6	8.2	47	7	US-11-370-584-2971
C 7	20.6	8.2	100	6	US-10-874-990B-90
C 8	20.6	8.2	112	8	US-11-266-748A-300647
C 9	20.4	8.1	68	8	US-11-194-055-199
C 10	20.4	8.1	86	8	US-11-194-055-198
C 11	20.4	8.1	86	8	US-11-194-055-177
C 12	20	7.9	80	8	US-11-169-140-46
C 13	20	7.9	80	8	US-11-191-244-63
C 14	20	7.9	95	8	US-11-169-140-47
C 15	20	7.9	95	8	US-11-191-244-64
C 16	20	7.9	115	9	US-11-348-413-10828
C 17	19.8	7.9	76	7	US-11-222-346A-42
C 18	19.8	7.9	110	8	US-11-366-748A-419451
C 19	19.6	7.8	98	9	US-11-365-556-80
C 20	19.6	7.8	98	9	US-11-365-556-81
C 21	19.6	7.8	98	9	US-11-365-556-83
C 22	19.4	7.7	47	7	US-11-370-584-995
C 23	19.4	7.7	102	7	US-11-244-330A-888

24	19.2	7.6	89	7	US-11-356-568A-42	Sequence 42, Appl
C 25	19.2	7.6	107	8	US-11-266-748A-411535	Sequence 411535, Ap
C 26	19.2	7.6	117	7	US-11-244-330A-6708	Sequence 6708, Ap
C 27	19	7.5	61	8	US-11-296-931-1	Sequence 1, Appl
C 28	19	7.5	118	7	US-11-314-834-4644	Sequence 4644, Ap
C 29	18.8	7.5	114	7	US-11-043-842-279	Sequence 279, App
C 30	18.6	7.4	99	8	US-11-217-529-173876	Sequence 173876, App
C 31	18.6	7.4	106	8	US-11-266-748A-420020	Sequence 420020, App
C 32	18.6	7.4	108	8	US-11-266-748A-232793	Sequence 232793, App
C 33	18.4	7.3	47	7	US-11-370-584-612	Sequence 612, App
C 34	18.4	7.3	51	8	US-11-143-642-1090	Sequence 1090, Ap
C 35	18.4	7.3	75	9	US-11-348-413-1748	Sequence 1748, Ap
C 36	18.4	7.3	77	6	US-10-834-268-4016	Sequence 4016, Ap
C 37	18.4	7.3	81	7	US-11-292-078-9878	Sequence 9878, Ap
C 38	18.4	7.3	103	8	US-11-266-748A-413307	Sequence 413307, Ap
C 39	18.4	7.3	109	7	US-11-244-330A-3545	Sequence 3545, Ap
C 40	18.4	7.3	113	9	US-11-348-413-9862	Sequence 9862, Ap
C 41	18.2	7.2	50	6	US-10-554-711-648	Sequence 648, App
C 42	18.2	7.2	50	6	US-10-554-759-648	Sequence 648, App
C 43	18.2	7.2	60	8	US-11-069-910-46	Sequence 46, Appl
C 44	18.2	7.2	99	6	US-10-531-545-10	Sequence 10, Appl
C 45	18.2	7.2	117	7	US-11-320-072-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-11-043-824-258/c
; Sequence 258, Application US/11043824
; Publication No. US20060172311A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847,1007
; CURRENT APPLICATION NUMBER: US/11/043,824
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 452
; SEQ ID NO 258
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-043-824-258

Query Match	8.7%;	Score 22;	DB 7;	Length 102;
Best Local Similarity	53.5%;	Pred. No. 3.8e+03;		
Matches	46;	Conservative	0;	Mismatches 40; Indels 0; Gaps 0;
QY	44	TTGGAAGGCGCTTTCCTTCTGATGTCAGAGTCTCTGACTCCCTCTGCCAGC	103	
Db	86	TTGAGGAGCGTTGGGCTCTTCTAGCTTCACGGGTACTCATTTGGCTGCTCCAGC	27	
QY	104	GGCTGAGTTCCGGGTCCTCCAGGTTCCG	129	
Db	26	GTCCGAGACATTTCTCCAGGTTTC	1	

RESULT 2
US-11-365-556-82
; Sequence 82, Application US/11365556
; Publication No. US20060166252A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROOKEY, KRISTIN L.
; APPLICANT: HOET, RENE
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
; TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
; TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS

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; FILE REFERENCE: DYAX/002
; CURRENT APPLICATION NUMBER: US/11/365,556
; CURRENT FILING DATE: 2006-02-28
; PRIOR APPLICATION NUMBER: US/03/837,306
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-365-556-82

Query Match      8.4%; Score 21.2; DB 9; Length 98;
Best Local Similarity 60.3%; Pred. No. 6.5e+03;
Matches 35; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 66 TTTTCTGGATGCAGTCTCTGACTCCCTCTGCCAGGGCTGAGTTTCGGGCTCCAG 123
Db 38 TCCTCCTGAAGCTGAGCTCTGTGCTGCGCAGACAGCGCCGTGTATTACTGTGCCAG 95

RESULT 3
US-11-370-584-3264/c
; Sequence 3264, Application US/11370584
; Publication No. US20060177863A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high
; FILE OF INVENTION: density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/11/370,584
; CURRENT FILING DATE: 2006-03-08
; PRIOR APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3264
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-2832-152 : polymorphic base C or T
US-11-370-584-3264

Query Match      8.3%; Score 21; DB 7; Length 47;
Best Local Similarity 91.3%; Pred. No. 5.8e+03;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 170 GCAGGAGGGCGGGGAGAGACG 192
Db 42 GCAGGAGGGCGGAGGAGACG 20

RESULT 4
US-11-266-748A-424752/c
; Sequence 424752, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
```

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; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 424752
; LENGTH: 103
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-424752

Query Match      8.3%; Score 21; DB 8; Length 103;
Best Local Similarity 66.7%; Pred. No. 7.5e+03;
Matches 30; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 69 TCTGGATGCAGTCTCTGACTCCCTCTGCCAGGGCTGAGTTT 113
Db 63 TCTTGTGGCGAGAACTGTGTTCTGTCTGCCCGCTGCTGCATT 19

RESULT 5
US-11-266-748A-307408
; Sequence 307408, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 307408
; LENGTH: 106
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; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 US-11-266-748A-307408

Query Match 8.3%; Score 20.8; DB 8; Length 106;
 Best Local Similarity 55.6%; Pred. No. 8.7e+03;
 Matches 40; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 59 GCTTCTGTTTTCTGGAGTCCTCTGAGTCCTCTGCTGCGGCTGAGTTCCGGC 118
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 15 GCTTGACTGTACAGCATGTTGTTTCTCTATCGCTCTGGGCTCAGGGCTTCATGTTCCGGT 74
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 119 TCCAGGTTCCGC 130
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 75 GACTGATTACCG 86
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RESULT 6
 US-11-370-584-2971
 ; Sequence 2971, Application US/11370584
 ; Publication No. US20060177863A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cohen, Daniel
 ; APPLICANT: Blumenfeld, Marta
 ; APPLICANT: Chumakov, Ilya
 ; TITLE OF INVENTION: Biallelic markers for use in constructing a high
 ; FILE OF INVENTION: density...
 ; FILE REFERENCE: GENSET.020CP1
 ; CURRENT APPLICATION NUMBER: US/11/370,584
 ; CURRENT FILING DATE: 2006-03-08
 ; PRIOR APPLICATION NUMBER: US/10/349,143
 ; PRIOR FILING DATE: 2003-01-21
 ; PRIOR APPLICATION NUMBER: US/09/422,978
 ; PRIOR FILING DATE: 1999-10-20
 ; PRIOR APPLICATION NUMBER: US 09/298,850
 ; PRIOR FILING DATE: 1999-04-21
 ; PRIOR APPLICATION NUMBER: US 60/109,732
 ; PRIOR FILING DATE: 1998-11-23
 ; PRIOR APPLICATION NUMBER: US 60/082,614
 ; PRIOR FILING DATE: 1998-04-21
 ; NUMBER OF SEQ ID NOS: 11796
 ; SEQ ID NO 2971
 ; LENGTH: 47
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; NAME/KEY: allele
 ; LOCATION: 24
 ; OTHER INFORMATION: 99-21310-416 : polymorphic base A or G
 US-11-370-584-2971

Query Match 8.2%; Score 20.6; DB 7; Length 47;
 Best Local Similarity 70.3%; Pred. No. 7.7e+03;
 Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 55 CTTTGCTTCTGTTTTCTGGATGCAGAGTCCTCTGACT 91
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 Db 5 CTCGTGCTCTTTTCTCTCTCCAGATCTCTCGGCT 41
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
 US-10-874-990B-90
 ; Sequence 90, Application US/10874990B
 ; Publication No. US20060216303A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SOMANTA LIMITED
 ; APPLICANT: do COUTO, Fernando J.R.
 ; APPLICANT: CERIANI, Roberto L.
 ; APPLICANT: PETERSON, Jerry A.
 ; APPLICANT: PADLAN, Eduardo A.
 ; TITLE OF INVENTION: PROCESSES AND PRODUCTS WITH MODIFIED ANTIBODIES OF HUMAN MILK FAT
 ; FILE REFERENCE: SOMA1140-4
 ; FILE REFERENCE: SOMA1140-4

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RESULT 9
US-11-194-055-199
; Sequence 199, Application US/11194055
; Publication No. US20060105360A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Liu, Chang-Gong
; APPLICANT: Calin, George, A.
; APPLICANT: Cinzia, Sevignani
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
; TITLE OF INVENTION: MICRORNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
; TITLE OF INVENTION: FEATURES
; FILE REFERENCE: 3589.1018-008
; CURRENT APPLICATION NUMBER: US/11/194,055
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: PCT/US2005/004865
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/543,119
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,929
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,963
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,940
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/580,959
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/580,797
; PRIOR FILING DATE: 2004-06-18
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 68
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-194-055-199

Query Match      8.1%; Score 20.4; DB 8; Length 68;
Best Local Similarity 61.1%; Pred. No. 9.9e+03;
Matches 33; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY      64  TGTTCCTGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGTGAGTTTCGG 117
Db      13  TGCATGGTGAGGGTGAGCTTCTGAAAACCCCTCCCATCATCGAGGGTTTGAG 66

RESULT 10
US-11-194-055-198
; Sequence 198, Application US/11194055
; Publication No. US20060105360A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Liu, Chang-Gong
; APPLICANT: Calin, George, A.
; APPLICANT: Cinzia, Sevignani
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
; TITLE OF INVENTION: MICRORNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
; TITLE OF INVENTION: FEATURES
; FILE REFERENCE: 3589.1018-008
; CURRENT APPLICATION NUMBER: US/11/194,055
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: PCT/US2005/004865
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/543,119
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,929
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,963
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/580,959
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/580,797
; PRIOR FILING DATE: 2004-06-18
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 86
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-194-055-198

Query Match      8.1%; Score 20.4; DB 8; Length 86;
Best Local Similarity 61.1%; Pred. No. 1.1e+04;
Matches 33; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY      64  TGTTCCTGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGTGAGTTTCGG 117
Db      22  TGCATGGTGAGGGTGAGCTTCTGAAAACCCCTCCCATCATCGAGGGTTTGAG 75

RESULT 11
US-11-194-055-277
; Sequence 277, Application US/11194055
; Publication No. US20060105360A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Liu, Chang-Gong
; APPLICANT: Calin, George, A.
; APPLICANT: Cinzia, Sevignani
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
; TITLE OF INVENTION: MICRORNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
; TITLE OF INVENTION: FEATURES
; FILE REFERENCE: 3589.1018-008
; CURRENT APPLICATION NUMBER: US/11/194,055
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: PCT/US2005/004865
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/543,119
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,929
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,963
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,940
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/580,959
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/580,797
; PRIOR FILING DATE: 2004-06-18
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 277
; LENGTH: 86
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-194-055-277

Query Match      8.1%; Score 20.4; DB 8; Length 86;
Best Local Similarity 61.1%; Pred. No. 1.1e+04;
Matches 33; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY      64  TGTTCCTGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGTGAGTTTCGG 117
Db      22  TGCATGGTGAGGGTGAGCTTCTGAAAACCCCTCCCATCATCGAGGGTTTGAG 75

RESULT 12
US-11-169-140-46/c
; Sequence 46, Application US/11169140
; Publication No. US20060099150A1
; GENERAL INFORMATION:
; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
```

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; PRIOR APPLICATION NUMBER: 60/580,959
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/580,797
; PRIOR FILING DATE: 2004-06-18
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 86
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-194-055-198
```

```
Query Match      8.1%; Score 20.4; DB 8; Length 86;
Best Local Similarity 61.1%; Pred. No. 1.1e+04;
Matches 33; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY      64  TGTTCCTGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGTGAGTTTCGG 117
Db      22  TGCATGGTGAGGGTGAGCTTCTGAAAACCCCTCCCATCATCGAGGGTTTGAG 75
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RESULT 11
US-11-194-055-277
; Sequence 277, Application US/11194055
; Publication No. US20060105360A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Liu, Chang-Gong
; APPLICANT: Calin, George, A.
; APPLICANT: Cinzia, Sevignani
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
; TITLE OF INVENTION: MICRORNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
; TITLE OF INVENTION: FEATURES
; FILE REFERENCE: 3589.1018-008
; CURRENT APPLICATION NUMBER: US/11/194,055
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: PCT/US2005/004865
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/543,119
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,929
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,963
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,940
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/580,959
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/580,797
; PRIOR FILING DATE: 2004-06-18
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 277
; LENGTH: 86
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-194-055-277
```

```
Query Match      8.1%; Score 20.4; DB 8; Length 86;
Best Local Similarity 61.1%; Pred. No. 1.1e+04;
Matches 33; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY      64  TGTTCCTGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGTGAGTTTCGG 117
Db      22  TGCATGGTGAGGGTGAGCTTCTGAAAACCCCTCCCATCATCGAGGGTTTGAG 75

RESULT 12
US-11-169-140-46/c
; Sequence 46, Application US/11169140
; Publication No. US20060099150A1
; GENERAL INFORMATION:
; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
```

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; APPLICANT: HOUSTON, Lou, L.
; APPLICANT: SHERIDAN, Philip, J.
; APPLICANT: HAWLEY, Stephen
; APPLICANT: GLYNN, Jacqueline, M.
; APPLICANT: CHAPIN, Steven
; TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CE
; TITLE OF INVENTION: BARRIERS
; FILE REFERENCE: 11474-037-999
; CURRENT APPLICATION NUMBER: US/11/169,140
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 60/267,601
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/248,819
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/248,478
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/237,929
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/949,039
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 09/969,748
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-11-169-140-46

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Query Match	7.9%	Score 20;	DB 8;	Length 80;
Best Local Similarity	58.3%	Pred. No. 1.4e+04;		
Matches	35;	Conservative	0;	Mismatches 25;
Indels	0;	Gaps	0;	

Qy 72 GGATGCAGAGTCCCTGTGACTCCCTCTGCCACGGGCTGAGTTTCGGGCTCCAGGTTCCGCGT 131

Db 80 GGGTCCCTGAGTCAGTCTCAGACGATCCGGCCACCGCCAGAGCCACCTCCGCGCTTGAAACCGCCCT 21

RESULT 13

```

US-11-191-244-63/c
; Sequence 63, Application US/11191244
; Publication No. US20060134103A1
; GENERAL INFORMATION:
; APPLICANT: HAWLEY, STEPHEN B.
; TITLE OF INVENTION: COMPOUNDS AND MOLECULAR COMPLEXES COMPRISING MULTIPLE
; TITLE OF INVENTION: BINDING REGIONS DIRECTED TO TRANSCYTOTIC LIGANDS
; FILE REFERENCE: 057220/1301
; CURRENT APPLICATION NUMBER: US/11/191,244
; CURRENT FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-11-191-244-63

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Query Match 7.9%; Score 20; DB 8; Length 80;

Best Local Similarity	58.3%	Pred. No. 1.4e+04;	
Matches	35;	Conservative	0; Mismatches 25; Indels 0; Gaps 0;

Qy 72 GGATGCAGAGTCCTCTGACTCCCTCTGCGCACGGGCTGAGTTTCGGGTCCAGGTTCCGGT 131

Dp 80 GGGTCTGAGTCAGTCAGAGATCGGTCACGGCCAGAGCCACTTCGCTCTGAACCGCCT 21

RESULT 14

US-11-169-140-47/c

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; Sequence 47, Application US/11169140
; Publication No. US20060099150A1
; GENERAL INFORMATION:
; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
; APPLICANT: HOUSTON, Lou, L.
; APPLICANT: SHERIDAN, Philip, J.
; APPLICANT: HAWLEY, Stephen
; APPLICANT: GLYNN, Jacqueline, M.
; APPLICANT: CHAPIN, Steven
; TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CEI
; TITLE OF INVENTION: BARRIERS
; FILE REFERENCE: 11474-037-999
; CURRENT APPLICATION NUMBER: US/11/169,140
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 60/267,601
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/248,819
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/248,478
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/237,929
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/949,039
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 09/969,748
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
; US-11-169-140-47

```

Query Match 7.9%; Score 20; DB 8; Length 95;

Best Local Similarity 58.3%; Pred. No. 1.5e+04;
Matches 35; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 72 GGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGCTGAGTTCCGGCTCCAGGTTCCGCGT 131

Db 95 GGGTCCCTGAGTCAGCTCAGACGATCCGGCCA CCGCAGAGGCCACTTCGCGCTGAACCGCCT 36

RESULT 15

US-11-191-244-64/c

US 1119124A ; Sequence 64, Application US/1119124A
US 20060134103A1 ; Publication No. US20060134103A1

: GENERAL INFORMATION:

APPLICANT: HAWLEY, STEPHEN B.

: TITLE OF INVENTION: COMPOUNDS AND MOLECULAR COMPLEXES COMPRISING MULTIPLE
: *****
: TITLE OF INVENTION: BINDING REGIONS DIRECTED TO TRANSCYTOTIC LIGANDS
: *****

FILE OF INVENTION
FILE REFERENCE: 057

CURRENT APPLICATION NUMBER: US/11/191,244

; CURRENT FILING DATE: 2005-07-27

; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 64

; LENGTH: 95

; TYPE: DNA

; ORGANISM: Artificial Sequences

FEATURE:

OTHER INFORMATION

Query Match 7.9†; Score 20; DB 8; Length 95;

Query Match	7.5%;	Score 20;	Length 10;
Best Local Similarity	58.3%;	Pred. No. 1.5e+04;	
Matches	35;	Conservative	0;
Mismatches	25;	Indels	0;
Gaps	0;		0;

QY 72 GGATGCAGAGTCTCTGACTCCCTCTGCCACGGGCTGAGTTTCGGGTCCAGGTTTCGGT 131

Search completed: October 16, 2006, 14:41:52
Job time : 1856 secs
